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(54) Title: CRYSTAL STRUCTURE OF BACE AND USES THEREOF

(57) Abstract: This invention is directed to the three dimensional crystal structure of Beta-site APP Cleaving Enzyme (BACE), and to the use of this structure in rational drug design methods to identify agents that may interact with active sites of BACE. Such agents may represent new therapeutics in the treatment and/or prevention of Alzheimer's Disease.

CRYSTAL STRUCTURE OF BACE AND USES THEREOF

Field of the Invention

[0001] The present invention relates to the three dimensional crystal structure of Beta-site APP Cleaving Enzyme (BACE), and to the use of this structure in rational drug design methods to identify agents that may interact with active sites of BACE. Such agents may represent new therapeutics in the treatment and/or prevention of Alzheimer's Disease.

Background of the Invention

[0002] A characteristic pathology of Alzheimer's Disease is the build up of insoluble amyloid plaques in the brain. These proteinaceous plaques are composed of a 4KDa, 42 amino acid fragment of β-Amyloid Precursor Protein (APP) and is termed Amyloid β-peptide (Aβ). The mechanism of Aβ production is hence of critical importance in understanding the onset and progress of Alzheimer's Disease. It has been shown that Aβ is derived from the proteolytic cleavage of a larger protein, β-amyloid precursor protein (APP). Two enzymes are responsible for this cleavage; first, the enzyme β-secretase cleaves APP at residue 671 (770aa isoform of APP numbering) and then γ-secretase cleaves at residue 716. More recently, the novel transmembrane aspartic protease BACE has been identified as being β-secretase. This protein is now a significant target in a therapeutic approach to Alzheimer's Disease. In rare cases of Alzheimer's Disease that are hereditary (Familial Alzheimer's Disease (FAD)) the disease phenotype has been isolated to mutations in the β-Amyloid Precursor Protein. One particular cohort, the 'Swedish mutation', exhibits a double mutation at the β-secretase cleavage site.

[0003] Based upon the role of BACE in Alzheimer's Disease, the elucidation of the three-dimensional structure of BACE, as well as its site of binding with APP, would have important implications in the treatment and/or prevention of Alzheimer's Disease and similar diseases associated with the

presence of insoluble amyloid plaques composed the 42 amino acid fragment of APP in the brain.

Summary of the Invention

[0004] The present invention provides a crystal of BACE complexed with an APP inhibitor peptide, as well as the three dimensional structure of BACE as derived by x-ray diffraction data of the BACE/APP inhibitor peptide crystal. Specifically, the three dimensional structure of BACE is defined by the structural coordinates shown in Figure 1, ± a root mean square deviation from the backbone atoms of the amino acids of not more than 1.5Å. The structural coordinates of BACE are useful for a number of applications, including, but not limited to, the visualization, identification and characterization of various active sites of BACE, and the BACE/APP inhibitor peptide complex, including the APP binding site. The active site structures may then be used to design various agents which interact with BACE, as well as BACE complexed with an APP protein or peptide, or related molecules.

[0005] The present invention is also directed to an active site of an APP binding protein or peptide, and preferably the APP peptide binding site of BACE that is elucidated and derived from the three dimensional structure of BACE as defined by the relative structural coordinates set forth in Figure 1, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

[0006] In one embodiment of the present invention, the active site of the APP binding protein or peptide, preferably the APP peptide binding site of BACE, comprises the relative structural coordinates according to Figure 1 of residues SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

[0007] In another embodiment, the active site of the APP binding protein or peptide, preferably the APP peptide binding site of BACE, comprises the

relative structural coordinates according to Figure 1 of residues LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYR129, VAL130, PRO131, TYR132, THR133, GLN134, GLY135, LYS136, TRP137, LYS168, PHE169, PHE170, ILE171, ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALA183, TYR184, ALA185, GLU186, ILE187, ALA188, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAL370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396 and ILE447, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

[0008] The present invention further provides a method for identifying an agent that interacts with an active site of BACE. The method comprises the steps of: (a) determining a putative active site of BACE from a three dimensional model of BACE using the relative structural coordinates of Figure 1, ± a root mean square deviation from the backbone atoms of the amino acids of not more than 1.5Å; and (b) performing various computer fitting analyses to identify an agent which interacts with the putative active site.

[0009] The present invention also provides method for identifying an agent that interacts with an active site of an APP binding protein or peptide, preferably BACE. The method comprises the steps of: (a) generating a three dimensional model of an active site of an APP binding protein or peptide using the relative structural coordinates according to Figure 1 of residues SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and (b) designing an agent using the three dimensional model generated in step (a).

[0010] The present invention also provides another method for identifying an agent that interacts with an active site of an APP binding protein or peptide, preferably BACE. The method comprises the steps of: (a) generating a three dimensional model of an active site of an APP binding protein or peptide using the relative structural coordinates according to Figure 1 of residues LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYR129, VAL130, PRO131, TYR132, THR133, GLN134, GLY135, LYS136, TRP137, LYS168, PHE169, PHE170, ILE171, ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALA183, TYR184, ALA185, GLU186, ILE187, ALA188, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAL370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396 and ILE447, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and (b) designing an agent using the three dimensional model generated in step (a).

[0011] Finally, the present invention provides agents, and preferably inhibitors, identified using the foregoing methods. Small molecules or other agents which inhibit or otherwise interfere with the ability of BACE to cleave APP may be useful in the treatment and/or prevention of Alzheimer's Disease.

[0012] Additional objects of the present invention will be apparent from the description which follows.

Brief Description of the Figure

[0013] Figure 1 provides the atomic structural coordinates for BACE and the APP inhibitor peptide as derived by X-ray diffraction of a crystal of the BACE and APP inhibitor peptide complex. "Atom type" refers to the atom whose coordinates are being measured. "Residue" refers to the type of residue of which each measured atom is a part - i.e., amino acid, cofactor, ligand or solvent. The

"x, y and z" coordinates indicate the Cartesian coordinates of each measured atom's location in the unit cell (Å). "Occ" indicates the occupancy factor. "B" indicates the "B-value", which is a measure of how mobile the atom is in the atomic structure ($Å^2$).

Detailed Description of the Invention

[0014] As used herein, the following terms and phrases shall have the meanings set forth below:

[0015] Unless otherwise noted, "BACE" is Beta-site APP Cleaving Enzyme, and is the β-secretase enzyme that cleaves β-amyloid precursor protein (APP) at residue 671 (770aa isoform of APP numbering). After cleavage of APP by BACE, the remaining APP is cleaved at residue 716 by γ-secretase, leaving a 42 amino acid fragment of APP that is found in the proteinaceous plaques of Alzheimer's patients. The amino acid sequence of BACE preferably has the amino acid sequence deposited with Swiss Prot under accession number P56817, including conservative substitutions. As used herein, BACE also includes "BACE peptides," which are molecules having less than the complete amino acid sequence of BACE. Preferably, BACE peptides include the active site in which BACE binds to and cleaves APP. Most preferably, the BACE peptide corresponds to amino acid residues 58-447 set forth in Figure 1 ("$BACE_{58-447}$"), including conservative substitutions.

[0016] "APP" is β-amyloid precursor protein having the amino acid sequence deposited with Swiss Prot under accession number CAA31830, including conservative substitutions. As used herein, APP also includes "APP peptides," which are molecules having less than the complete amino acid sequence of APP. Preferably, APP peptides include the active site in which APP is cleaved by BACE.

[0017] An "APP inhibitor peptide" is a peptide which inhibits binding between BACE and APP. Preferably, the APP peptide has the amino acid sequence SER-GLU-VAL-ASN-Sta-VAL-ALA-GLU-PHE, where Sta is rare amino acid (S)-Statine.

[0018] An "APP binding protein or peptide" is a protein or peptide that binds APP and has a APP binding site, and includes but is not limited to BACE and BACE peptides.

[0019] Unless otherwise indicated, "protein" shall include a protein, protein domain, polypeptide or peptide.

[0020] "Structural coordinates" are the Cartesian coordinates corresponding to an atom's spatial relationship to other atoms in a molecule or molecular complex. Structural coordinates may be obtained using x-ray crystallography techniques or NMR techniques, or may be derived using molecular replacement analysis or homology modeling. Various software programs allow for the graphical representation of a set of structural coordinates to obtain a three dimensional representation of a molecule or molecular complex. The structural coordinates of the present invention may be modified from the original set provided in Figure 1 by mathematical manipulation, such as by inversion or integer additions or subtractions. As such, it is recognized that the structural coordinates of the present invention are relative, and are in no way specifically limited by the actual x, y, z coordinates of Figure 1.

[0021] An "agent" shall include a protein, polypeptide, peptide, nucleic acid, including DNA or RNA, molecule, compound or drug.

[0022] "Root mean square deviation" is the square root of the arithmetic mean of the squares of the deviations from the mean, and is a way of expressing deviation or variation from the structural coordinates of BACE described herein. The present invention includes all embodiments comprising conservative substitutions of the noted amino acid residues resulting in same structural coordinates within the stated root mean square deviation.

[0023] The numbering of the amino acid residues identified in Figure 1 are based on the numbering of the full length BACE protein from the start of the signal sequence. It will be obvious to the skilled practitioner that the numbering of the amino acid residues of BACE may be different than that set forth herein or may contain certain conservative amino acid substitutions that yield the same

three dimensional structures as those defined in Figure 1. Corresponding amino acids and conservative substitutions in other isoforms or analogues are easily identified by visual inspection of the relevant amino acid sequences or by using commercially available homology software programs (e.g., MODELLAR, MSI, San Diego, CA).

[0024] "Conservative substitutions" are those amino acid substitutions which are functionally equivalent to the substituted amino acid residue, either by way of having similar polarity, steric arrangement, or by belonging to the same class as the substituted residue (e.g., hydrophobic, acidic or basic) and includes substitutions having an inconsequential effect on the three dimensional structure of BACE, with respect to the use of this structure for the identification and design of agents which interact with BACE, for molecular replacement analyses and/or for homology modeling.

[0025] As used herein, an "active site" refers to a region of a molecule or molecular complex that, as a result of its shape and charge potential, favorably interacts or associates with another agent (including, without limitation, a protein, polypeptide, peptide, nucleic acid, including DNA or RNA, molecule, compound, antibiotic or drug) via various covalent and/or non-covalent binding forces. Preferably, the active site of BACE corresponds to the site in which BACE cleaves the APP molecule.

[0026] As such, the active site of BACE may include, for example, both the actual site in which BACE binds and cleaves APP, as well as accessory binding sites adjacent or proximal to the actual binding site that nonetheless may affect the ability of BACE to bind and cleave APP, either by direct interference with the actual site of binding or by indirectly affecting the steric conformation or charge potential of the BACE molecule and thereby preventing or reducing the ability of BACE to bind to APP at the actual binding site. As used herein, an active site also includes BACE or BACE analog residues which exhibit observable NMR perturbations in the presence of a binding ligand, such as APP or an APP peptide. While such residues exhibiting observable NMR perturbations may not necessarily be in direct contact with or immediately

proximate to ligand binding residues, they may be critical to BACE residues for rational drug design protocols.

[0027] The present invention is directed to a crystallized complex of BACE and an APP inhibitor peptide that effectively diffracts X-rays for the determination of the structural coordinates of the complex. As used herein, BACE preferably corresponds to $BACE_{58-447}$ as set forth in Figure 1, with the N-terminal domain consisting of amino acid residues 58-207 shown in Figure 1, and the C-terminal domain consisting of amino acid residues 208-447 shown in Figure 1. The APP inhibitor peptide is preferably SER-GLU-VAL-ASN-Sta-VAL-ALA-GLU-PHE.

[0028] Using the crystal complex of the present invention, X-ray diffraction data can be collected by a variety of means in order to obtain the atomic coordinates of the crystallized molecule or molecular complex. With the aid of specifically designed computer software, such crystallographic data can be used to generate a three dimensional structure of the molecule or molecular complex. Various methods used to generate and refine the three dimensional structure of a crystallized molecule or molecular structure are well known to those skilled in the art, and include, without limitation, multiwavelength anomalous dispersion (MAD), multiple isomorphous replacement, reciprocal space solvent flattening, molecular replacement, and single isomorphous replacement with anomalous scattering (SIRAS).

[0029] Accordingly, the present invention also provides the three dimensional structure of BACE as derived by x-ray diffraction data of the BACE/APP inhibitor peptide crystal. Specifically, the three dimensional structure of BACE is defined by the structural coordinates shown in Figure 1, ± a root mean square deviation from the backbone atoms of the amino acids of not more than 1.5Å, preferably not more than 1.0Å, and most preferably not more than 0.5Å. The structural coordinates of BACE are useful for a number of applications, including, but not limited to, the visualization, identification and characterization of various active sites of BACE, and the BACE/APP inhibitor peptide complex, including the APP or APP peptide binding site. The active site

structures may then be used to design agents with interact with BACE, as well as BACE complexed with APP, an APP peptide or related molecules.

[0030] The present invention is also directed to an active site of an APP binding protein or peptide, preferably the APP peptide binding site of BACE, which comprises the relative structural coordinates according to Figure 1 of residues SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, more preferably not more than 1.0Å, and most preferably not more than 0.5Å.

[0031] In another preferred embodiment, the active site of an APP binding protein or peptide, preferably the APP peptide binding site of BACE, comprises the relative structural coordinates according to Figure 1 of residues LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYR129, VAL130, PRO131, TYR132, THR133, GLN134, GLY135, LYS136, TRP137, LYS168, PHE169, PHE170, ILE171, ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALA183, TYR184, ALA185, GLU186, ILE187, ALA188, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAL370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396 and ILE447, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, more preferably not more than 1.0Å, and most preferably not more than 0.5Å.

[0032] Another aspect of the present invention is directed to a method for identifying an agent that interacts with an active site of BACE comprising the steps of: (a) determining an active site of BACE from a three dimensional model of BACE using the relative structural coordinates of Figure 1, ± a root mean square deviation from the backbone atoms of said amino acids of not more than

1.5Å, more preferably not more than 1.0Å, and most preferably not more than 0.5Å; and (b) performing computer fitting analysis to identify an agent which interacts with said active site. Computer fitting analyses utilize various computer software programs that evaluate the "fit" between the putative active site and the identified agent, by (a) generating a three dimensional model of the putative active site of a molecule or molecular complex using homology modeling or the atomic structural coordinates of the active site, and (b) determining the degree of association between the putative active site and the identified agent. Three dimensional models of the putative active site may be generated using any one of a number of methods known in the art, and include, but are not limited to, homology modeling as well as computer analysis of raw data generated using crystallographic or spectroscopy data. Computer programs used to generate such three dimensional models and/or perform the necessary fitting analyses include, but are not limited to: GRID (Oxford University, Oxford, UK), MCSS (Molecular Simulations, San Diego, CA), AUTODOCK (Scripps Research Institute, La Jolla, CA), DOCK (University of California, San Francisco, CA), Flo99 (Thistlesoft, Morris Township, NJ), Ludi (Molecular Simulations, San Diego, CA), QUANTA (Molecular Simulations, San Diego, CA), Insight (Molecular Simulations, San Diego, CA), SYBYL (TRIPOS, Inc., St. Louis. MO) and LEAPFROG (TRIPOS, Inc., St. Louis, MO).

[0033] The present invention also provides a method for identifying an agent that interacts with an active site of an APP binding protein or peptide, and preferably the APP peptide binding site on BACE. The method comprises the steps of: (a) generating a three dimensional model of an active site of an APP binding protein or peptide using the relative structural coordinates according to Figure 1 of residues SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, more preferably not more than 1.0Å, and most preferably not more than 0.5Å;

and (b) designing an agent using the three dimensional model generated in step (a). In another preferred embodiment, the active site of the APP binding protein or peptide is generated using the three dimensional model defined by the relative structural coordinates according to Figure 1 of residues LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYR129, VAL130, PRO131, TYR132, THR133, GLN134, GLY135, LYS136, TRP137, LYS168, PHE169, PHE170, ILE171, ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALA183, TYR184, ALA185, GLU186, ILE187, ALA188, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAL370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396 and ILE447, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, more preferably not more than 1.0Å, and most preferably not more than 0.5Å.

[0034] The effect of such an agent identified by computer fitting analyses on the APP binding protein or peptide may be further evaluated by obtaining or synthesizing the agent, and contacting the identified agent with the APP binding protein or peptide in order to determine the effect the agent has on the APP binding protein or peptide. Preferably, the APP binding protein or peptide is BACE (or a BACE peptide), and the agent is a potential inhibitor of binding between BACE (or a BACE peptide) and APP (or an APP peptide). Therefore, in the preferred embodiment, the agent is contacted with BACE (or a BACE peptide) in the presence of APP (or a APP peptide), to determine the ability of the agent to inhibit binding between BACE (or the BACE peptide) and APP (or the APP peptide). Depending upon the action of the agent on the active site, the agent may act either as an inhibitor or activator of the BACE/APP binding. Assays may be performed and the results analyzed to determine whether the agent is an inhibitor (i.e., the agent may reduce or prevent binding affinity between BACE and APP), an activator (i.e., the agent may increase binding

affinity between BACE and APP), or has no effect on the interaction between BACE and APP. Agents identified using the foregoing methods, and preferably inhibitors of BACE cleavage of APP, may then be tested as therapeutics in the treatment and/or prevention of Alzheimer's Disease, and other diseases that are also characterized by the presence of the 42 amino acid fragment of APP in the proteinaceous plaques of the brain.

[0035] Various molecular analysis and rational drug design techniques are further disclosed in U.S. Patent Nos. 5,834,228, 5,939,528 and 5,865,116, as well as in PCT Application No. PCT/US98/16879, published WO 99/09148, the contents of which are hereby incorporated by reference.

[0036] Finally, the present invention is also directed to the agents, and preferably the inhibitors, identified using the foregoing methods. Such agents may be a protein, polypeptide, peptide, nucleic acid, including DNA or RNA, molecule, compound, or drug, and preferably are small molecules that effectively inhibit binding between BACE and APP or an APP peptide. Such molecules may be useful in treating, preventing or inhibiting progression of Alzheimer's Disease.

[0037] The present invention may be better understood by reference to the following non-limiting Example. The following Example is presented in order to more fully illustrate the preferred embodiments of the invention, and should in no way be construed as limiting the scope of the present invention.

Example 1

A. Methods

[0038] Cloning of Human BACE1. Human polyA+ mRNA from whole brain (Clontech) was converted to cDNA by random-priming using Thermoscript RT-PCR System, according to the manufacturer's protocol (Lifetechnologies). This cDNA was amplified by PCR using the forward and reverse primers, 5' GCTCTAGAACCCAGC ACGGCATCCGGCTG 3' (XbaI site indicated by underlined sequence; nts. 517-537 in accession no. AF190725) and 5' CCAAGCATGCGGCCGCAATAGGCTATGGTCA TGAGGGTTGAC 3' (NotI site

indicated by underlined sequence; nts. 1809-1833; bold "A" indicates additional nucleotide to permit in-frame translation of the Fc chimera; see below), respectively. PCR was accomplished using Expand Long Polymerase kit according to the manufacturer's conditions (Roche Biochemicals; buffer #3), with PCR cycling consisting of an initial denaturing step at 95°C for 3min, 30-40 cycles of denaturation at 94°C for 30sec, annealing at 65°C for 30sec, elongation at 68°C for 1min 30sec, followed by a final elongation at 68°C for 5min. The PCR products were run on a 1% agarose gel. The appropriate band was cut out of the gel, purified by Quantum Prep Freeze 'N Squeeze DNA Extraction Columns (Bio-Rad), and cloned into the SpeI/NotI sites of the mammalian expression vector, pED/Fc (Kaufman, RJ et al., 1991, Nucl. Acids. Res. 19:4485-4490).

[0039] An intermediate construct contained the honey bee meletin secretory leader fused to the the prodomain and coding region of BACE1, just upstream to the predicted transmembrane domain of BACE1 (Vassar, R. et al., 1999, Science 286:735-741). The absence of the predicted hydrophobic transmembrane domain in this construct would permit soluble secreted BACE.Fc protein to be extracted from the conditioned medium. Downstream of BACE1 was an engineered enterokinase cleavage site followed by sequence encoding the Fc portion of immunoglobulin IgG. The final construct contained the BACE1.Fc gene, flanked by SalI and EcoRI in pED/Fc, cloned into the SalI/EcoRI sites of the mammalian expression vector, pHTop, a derivative of pED, in which the majority of the adenovirus major late promoter was replaced by six repeats of a bacterial tetracycline operator (described in Gossen et al, 1992, PNAS, 89:5547-5551). Sequencing of the BACE1.Fc recombinant gene was accomplished by BigDye terminator dideoxy sequencing using an ABI3700. Sequence analyses was accomplished using DNAstar software package.

[0040] Expression of Human BACE1. The vector, pHTOP, with the BACE1.Fc insert, contains the dihydrofolate reductase gene and when introduced in the cell line CHO/A2 (see description below) functions very

efficiently and high expressers can be selected by isolating cells surviving in high methotrexate concentrations.The CHO/A2 cell line is derived from CHO DUKX B11 (Urlaub and Chasin, 1980, PNAS USA 77:4216-4220) by stably integrating a transcriptional activator (tTA), a fusion protein between the Tet repressor and the herpes virus VP16 transcriptional domain (Gossen et al). A CHO cell line expressing extracellular BACE1.Fc was established by transfecting (lipofection) pHTopBACE1.Fc into CHO/A2 cells and selecting clones in 0.02 and 0.05 μM methotrexate. The conditioned media from multiple clones were screened by Western blot using a (mouse) anti-human IgG.Fc HRP antibody. The same clones were also metabolically labeled with 35 S (met/cys). The best clone, determined by virtue of its high expression, was one which resulted from 0.05 μM MTX selection and was chosen to be scaled up for roller bottle conditioned media production (4 Liters). The conditioned media was then used for purification. The expressed protein has residues 22-460 and nine extra residues at the C-terminal (an artefact from cloning and remains of the EK cleavage site).

[0041] Purification of BACE1. For the purification of BACE the 102 liters of conditioned media was used. During purification the activity of the enzyme was estimated at room temperature by continuously monitoring the fluorescent intensity for 5-10 min. at 420 nm (ext – 320 nm) Abz-Ser-Glu-Val-Asn-Leu-Asp-Ala-Glu-Phe-Arg-Dpa (Abz = Amino benzoic acid, Dpa = 9,10-diphenylanthracene) as the substrate. The reaction mixture contained 20 μM of substrate, different amounts of enzyme in 0.5 ml of 20 mM Tris-HCl pH 8.0 and 100 mM NaCl. The concentrated material of conditioned media(1.6 l) was applied to column (2.8 x 12 cm) containing ImmunoPure Immobilized Protein A agarose (Pierce, Il, USA) equilibrated in PBS buffer. The speed of application was 2 ml/min. The column was washed with 1 litre of PBS buffer and the BACE-Fc protein was eluted by ImmunoPure IgG Elution Buffer (Pierce, Il, USA). The fractions containing protein were immediately neutralized by 1 M Tris-HCl to pH 8.0.

[0042] The obtained protein material was treated with Enterokinase at 25°C. The ratio of BACE-Fc to Enterokinase was 3000:1 and the time of reaction was 3 hrs. The reaction was stopped by removing Enterokinase from reaction mixture by applying the protein to a column (1 x 5 cm) containing soybean trypsin inhibitor agarose (Sigma, Mo, USA) equilibrated in 20 mM Tris-HCL pH 8.0 containing 100 mM NaCl (speed was 1 ml/min). The flow through material contained BACE and cleaved Fc. Cleaved Fc was removed from BACE by flowing through a protein A column equilibrated in 20 mM Tris-HCl pH 8.0.

[0043] BACE was partially de-glycosylated using PNGase F (New England Labs., Ma, USA). 8-9 μg of PNGase was added to 1 mg of BACE and the incubation was carried at 37° C for 16 hrs. The additional 5-6 μg of PNGase was added to each mg of BACE and incubation was continued for another 4 hrs. The purified BACE was separated from PNGase by HPLC size-exclusion chromatography using 21.5 x 30 cm G-3000SW column (TosoHaas, Pa, USA) equilibrated in 20 mM tris-HCL pH 8.0 containing 200 mM NaCl. (Speed of elution was 3 ml/min). The purified BACE was concentrated and used for crystallization experiments.

[0044] N-terminal sequencing of purified BACE reveals a mixture of protein species, with the major sample having the processing domain cleaved and beginning at residue 47 (all numbering refers to full length BACE;accession code: A59090) and a minor sample which had not been cleaved beginning at residue 22. A smaller sample with sequence MTIAY was also detected.

[0045] Crystallization. The crystals were grown using the hanging drop vapour diffusion method. The protein was concentrated to mg/ml in 20mM Tris pH 7.5, 200mM sodium chloride. Inhibitor peptide sequence is SEVNStaVAEF, where Sta is the rare amino acid (*S*)-Statine. It was concentrated to 100mM in 100% DMSO and mixed with concentrated protein in a two-fold peptide excess to form the complex. 1 μl of complex was added to 1 μl of well solution containing 100mM Sodium Cacodylate pH6.5, 25% PEG8K, 300mM lithium sulphate. Plate-like crystal clusters grew within one week to dimensions of 200

μm x 400 μm x 75 μm. Single crystals were transferred to a stabilizing, cryoprotectant solution which contained the well solution plus 25% Glycerol for a brief, 10 second, soak and then frozen in liquid nitrogen. X-ray diffraction crystals had space group I222, and unit cell parameters a=86.627, b=130.861, c=130.729, and $\alpha = \beta = \gamma = 90°$.

B. Results

[0046] Structure Determination and Overall Fold. Full length BACE was expressed in CHO cells as a fc fusion protein and, after purification, cleavage and partial deglycosylation, complexed with peptide inhibitor and crystallized. Crystals diffracted to 2.3Å and the structure was solved using the technique of molecular replacement. The search model used was derived from cod atlantic Pepsin and contained 63% of the final number of atoms. The density modified maps obtained using a poly-alanine version of the search model (39% of the final atoms) provided sufficient information to build all but 12 amino acids. The final model contains residues from 59 to 448 (using full length numbering), all 9 residues of the statine inhibitor and 360 water molecules. Of the four predicted N-linked glycosylation sites only two have interpretable electron density.

[0047] The overall shape of the BACE protein is spherical and is composed of two distinct domains, an N-terminal (58-207) and a C-terminal (208-447). With the first thirteen amino acids (58-71) being packed against residues 238-243. There is a significant cleft-like channel across one surface of the interface between the domains. This contains the inhibitor peptide and conserved aspartic acid motifs that define the active sites of aspartic proteases.

[0048] The N-terminal domain is composed of a single a-helix preceeding the loop joining the two domains and thirteen β-strands. The larger C-terminal domain has a total of seventeen β-strands and three α-helices. The overall topology is characterised by an eight stranded antiparallel interdomain β-sheet. This central sheet comprises the majority of the active site residues including the two conserved aspartates (one from each domain:93 and 289). Asp93 and

Asp289 define the position of a pseudo two-fold axis for the central β-sheet. Outside of this symmetry the two domains differ significantly. The N-terminal domain has an extra two strands extending the central sheet. In addition, there are two anti-parallel β-sheets above and below the central sheet composed of three and four β-strands respectively. Residues from the upper sheet (131-135) fold over the active site aspartates and form a 'flap' over the centre of the peptide binding cleft.

[0049] The C-terminal domain contains two lobes in addition to the strands which from the central β-sheet. These are weakly homologous to known aspartic protease structures. The binding pocket for the P1` and P3` positions are instead derived from three β-turns 388-391, 284-286 and 255-261.

[0050] There are a total of six cysteine residues in BACE. Each of these is involved in a disulphide interaction. The pattern of disulphide crosslinking, Cys278-Cys443, Cys380-Cys330, Cys420-Cys216 are unique in the aspartic proteases known to date.

[0051] A novel aspartic protease. The first attempts to study the relationship of function to structure of an Apartic proteases began in the 1930s with Pepsin. Since then this rich field of research has been successfully applied to the design of clinically used inhibitors in only one system; HIV protease. The reasons for this are related more to the validity of the pharmacological target than the efficacy of inhibitors. β-secretase has been described as a novel protease and has been shown to be linked to the onset and progression of Alzheimer's disease.

[0052] From a gross viewpoint the overall fold and domain organization is very similar to that of a canonical aspartic protease. The comparison at a more detailed level reveals a significant number of differences. The active site is characterized by two aspartic residues surrounded by a conserved set of hydrogen bonds termed a 'fireman's grip'. This is reproduced in the -secretase structure presented here. The characteristic flap which wraps over the active site in pepsin is absent from the C-terminal domain in a manner analogous to

cathepsin D. In β-secretase the critical main chain amide hydrogen bond to the carboxyl group of statine is maintained by Thr133 from this flap. The amide of the statine makes a hydrogen bond to the carboxyl group of Gly95, emphasizing that the statine residue occupies both the P1 and P1` position.

[0053] Enzyme Mechanism. It has been shown that β-secretase cleavage is dependent on proximity to the cell membrane. Both β-secretase and its substrate APP have putative transmembrane regions. Our expressed BACE construct finishes one amino acid before the predicted transmembrane region. The final residue in the current structure is Ile447, thirteen residues away from the beginning of the putative transmembrane domain. In the current crystal structure Ile447 is only 6Å away from the P3 Glutamic acid of the inhibitor suggesting a role for the remaining C-terminal residues in the enzyme mechanism. The Statine residue of the inhibitor peptide is bound at the S1 position within the active site. The position of the C-3 hydroxyl group, coplanar to and within hydrogen bonding distance of both aspartate 93 and 289 carboxyl groups, confirms that the rare amino acid mimics the tetrahedral transition state i.e the intermediate of peptide-bond hydrolysis. The distance between the oxygen atoms of Asp93 and Asp289 is 2.8Å, strongly suggesting a shared proton atom and a classic aspartic protease pK profile for these side-chains and a common enzyme mechanism to other known aspartic proteases.

[0054] Inhibitor binding. The inhibitor peptide binds in an extended form along a 20Å groove formed at the interface between the domains. The conserved catalytic aspartic residues lie at the middle of this groove. The bound peptide consists of 8 amino acids plus a statine amino acid at position 5. There is contiguous electron density for the whole peptide. The statine based inhibitor used in this study has been show to inhibit the β-secretase enzyme with nanomolar efficiency. The peptide sequence is based on the P10 to P4` APP751 Sweedish family mutation. This mutation of a Lys-Asn at the P2 position and Met-Leu at the P1 position is strongly correlated to the early onset of

Alzheimer's disease. The inhibitor peptide utilizes Statine's Leucyl like side-chain to explore this interaction. Due to the di-peptide nature of Satine the P1` position of the substrate is shifted to P2` leaving an empty S1` pocket. The β-secretase enzyme appears to have a novel preference for an apartate or glutamate at the P1` position whereas other aspartic proteases show a preference for hydrophobic residues. This unusual preference for a negatively charged P1' amino acid is explained by the guanadinium group of Arg189 forming part of the putative S1` pocket. Even at the acidic pH optima of BACE the arginine side chain would form a positively charged environment for the possibly protonated carboxyl side-chain atoms.

[0055] The S1 and S3 binding pockets are a contiguous, hydrophobic pocket formed by the side-chain of residues Tyr132, Phe169, Ile171, Trp176, Ile179 and main chain atoms of Gly74, and Gln73. This packing of inhibitor P1 and P3 side chains has been seen in previous aspartic protease complexes.

[0056] The canonical APP cleavage site for b-secretase appears to have a preference for a small hydrophobic residues at the P2` position. The side chain of the valine residue bound in the putative S2` site of β-secretase appears to not make any significant interactions with the protein, its main chain however forms a tight set of hydrogen bonds to the backbone carboxyl of Gly 95 and the sidechain OH of Tyr259. In turn, Tyr259 is held rigidly in place by an edge-pi interaction with Trp258, which packs against the guanadinium group of Arg256.

[0057] *Swedish mutation. Autosomal dominant mutations identified on* the β-amyloid precusor protein have been correlated to early-onset cases of Alzheimer's disease. These have been shown to cluster around the three canonical cleavage sites. A double (the so-called Swedish) mutation of Lys670-Met671 (770aa isoform of APP numbering) to Asn-Leu causes an increase in the overall quantity of Aβ detectable in the plasma and in the medium of cultured fibroblasts from carriers of the Swedish mutation. These two amino acids lie at the P2 and P1 positions of the β-secretase active site. The statine based inhibitor used here is based on this Swedish mutation. A methionine at position

P1 would clearly be accommodated but would loose the van Der Waal's complentarity exhibited by the statine side-chain to Leu90 and Ile178. The Cϵ atom of the methione would make supplement the hydrophobic interaction to Phe169.

Table 1

Residues of BACE Within 4Å of Peptide Inhibitor

SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296, ARG368

Residues of BACE Within 8Å of Peptide Inhibitor

LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYR129, VAL130, PRO131, TYR132, THR133, GLN134, GLY135, LYS136, TRP137, LYS168, PHE169, PHE170, ILE171, ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALA183, TYR184, ALA185, GLU186, ILE187, ALA188, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAL370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396, ILE447

[0058] All publications mentioned herein above, whether to issued patents, pending applications, published articles, deposited sequences, or otherwise, are hereby incorporated by reference in their entirety. While the foregoing invention has been described in some detail for purposes of clarity and understanding, it will be appreciated by one skilled in the art from a reading of the disclosure that various changes in form and detail can be made without departing from the true scope of the invention in the appended claims.

What is claimed is:

1. A crystallized complex of Beta-site APP Cleaving Enzyme (BACE) and SER-GLU-VAL-ASN-Sta-VAL-ALA-GLU-PHE.

2. The crystallized complex of Claim 1, wherein BACE has an N-terminal domain consisting of amino acid residues 58-207 shown in Figure 1, and a C-terminal domain consisting of amino acid residues 208-447 shown in Figure 1.

3. An active site of an APP binding protein or peptide comprising the relative structural coordinates according to Figure 1 of residues SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

4. The active site of Claim 3, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0Å.

5. The active site of Claim 3, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5Å.

6. An active site of an APP binding protein or peptide comprising the relative structural coordinates according to Figure 1 of residues LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYR129, VAL130, PRO131, TYR132, THR133, GLN134, GLY135, LYS136, TRP137, LYS168, PHE169, PHE170, ILE171,

ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALA183, TYR184, ALA185, GLU186, ILE187, ALA188, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAL370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396 and ILE447, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

7. The active site of Claim 6, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0Å.

8. The active site of Claim 6, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5Å.

9. A method for identifying an agent that interacts with an active site of Beta-site APP Cleaving Enzyme (BACE), comprising the steps of:

(a) determining an active site of BACE from a three dimensional model of BACE using the relative structural coordinates of Figure 1, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and

(b) performing computer fitting analysis to identify an agent which interacts with said active site.

10. The method of Claim 9, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0Å.

11. The method of Claim 9, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5Å.

12. A method for identifying an agent that interacts with an active site of an APP binding protein or peptide, comprising the steps of:

(a) generating a three dimensional model of an active site of an APP binding protein or peptide using the relative structural coordinates according to Figure 1 of residues SER71, GLY72, LEU91, ASP93, GLY95, SER96, VAL130, PRO131, TYR132, THR133, GLN134, ILE171, ILE179, ILE187, ALA188, ARG189, PRO190, TRP258, TYR259, ASP284, LYS285, ASP289, GLY291, THR292, THR293, ASN294, ARG296 and ARG368, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and

(b) designing an agent using the three dimensional model generated in step (a).

13. The method of Claim 12, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0Å.

14. The method of Claim 12, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5Å.

15. The method of Claim 12, wherein the agent is designed by performing computer fitting analysis of the agent with the three dimensional model generated in step (a).

16. The method of Claim 12, further comprising the steps of: (c) obtaining or synthesizing the agent so designed; and (d) contacting the agent with the APP binding protein or peptide in order to determine the effect the agent has on the APP binding protein or peptide.

17. The method of Claim 12, wherein the APP binding protein or peptide is BACE.

18. The method of Claim 17, wherein the agent is a potential inhibitor of binding between BACE and APP.

19. The method of Claim 18, further comprising the steps of: (c) obtaining or synthesizing the agent so designed; and (d) contacting the agent with BACE in the presence of APP.

20. A method for identifying an agent that interacts with an active site of an APP binding protein or peptide, comprising the steps of:

(a) generating a three dimensional model of an active site of an APP binding protein or peptide using the relative structural coordinates according to Figure 1 of residues LYS70, SER71, GLY72, GLN73, GLY74, TYR75, LEU91, VAL92, ASP93, THR94, GLY95, SER96, SER97, ASN98, TYR129, VAL130, PRO131, TYR132, THR133, GLN134, GLY135, LYS136, TRP137, LYS168, PHE169, PHE170, ILE171, ASN172, SER174, TRP176, GLY178, ILE179, LEU180, GLY181, ALA183, TYR184, ALA185, GLU186, ILE187, ALA188, ARG189, PRO190, ASP191, ASP192, ARG256, TRP258, TYR259, TYR283, ASP284, LYS285, SER286, ILE287, VAL288, ASP289, SER290, GLY291, THR292, THR293, ASN294, LEU295, ARG296, GLY325, GLU326, ARG368, VAL370, LYS382, PHE383, ALA384, ILE385, SER386, GLN387, SER388, SER389, THR390, GLY391, THR392, VAL393, GLY395, ALA396 and ILE447, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and

(b) designing an agent using the three dimensional model generated in step (a).

21. The method of Claim 18, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0Å.

22. The method of Claim 20, wherein the ± a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5Å.

23. The method of Claim 20, wherein the agent is designed by performing computer fitting analysis of the agent with the three dimensional model generated in step (a).

24. The method of Claim 20, further comprising the steps of: (c) obtaining or synthesizing the agent so designed; and (d) contacting the agent with the APP binding protein or peptide in order to determine the effect the agent has on the APP binding protein or peptide.

25. The method of Claim 20, wherein the APP binding protein or peptide is BACE.

26. The method of Claim 25, wherein the agent is a potential inhibitor of binding between BACE and APP.

27. The method of Claim 26, further comprising the steps of: (c) obtaining or synthesizing the agent so designed; and (d) contacting the agent with BACE in the presence of APP.

28. An agent identified by the method of Claim 9.

29. An agent identified by the method of Claim 12.

30. An agent identified by the method of Claim 20.

Figure 1

		Atom Type	Res.			X	Y	Z		
ATOM	1	N	GLY	A	58	31.563	49.775	16.324	1.00	59.33
ATOM	2	CA	GLY	A	58	32.861	50.358	16.764	1.00	58.44
ATOM	3	C	GLY	A	58	33.594	49.446	17.727	1.00	57.81
ATOM	4	O	GLY	A	58	34.067	48.331	17.333	1.00	56.66
ATOM	5	N	SER	A	59	33.712	49.888	18.975	1.00	56.66
ATOM	6	CA	SER	A	59	34.391	49.094	20.015	1.00	55.45
ATOM	7	C	SER	A	59	33.560	49.088	21.293	1.00	53.77
ATOM	8	O	SER	A	59	32.978	50.147	21.704	1.00	54.40
ATOM	9	CB	SER	A	59	35.781	49.668	20.309	1.00	55.79
ATOM	10	OG	SER	A	59	35.690	50.952	20.899	1.00	57.07
ATOM	11	N	PHE	A	60	33.480	47.924	21.927	1.00	49.96
ATOM	12	CA	PHE	A	60	32.719	47.772	23.181	1.00	45.72
ATOM	13	C	PHE	A	60	33.681	47.269	24.247	1.00	44.79
ATOM	14	O	PHE	A	60	33.495	46.160	24.831	1.00	45.45
ATOM	15	CB	PHE	A	60	31.564	46.790	22.976	1.00	43.28
ATOM	16	CG	PHE	A	60	30.557	47.249	21.957	1.00	41.00
ATOM	17	CD1	PHE	A	60	30.875	47.267	20.602	1.00	40.54
ATOM	18	CD2	PHE	A	60	29.301	47.701	22.355	1.00	40.58
ATOM	19	CE1	PHE	A	60	29.954	47.731	19.658	1.00	39.88
ATOM	20	CE2	PHE	A	60	28.375	48.166	21.419	1.00	39.50
ATOM	21	CZ	PHE	A	60	28.704	48.182	20.070	1.00	39.23
ATOM	22	N	VAL	A	61	34.709	48.073	24.500	1.00	43.29
ATOM	23	CA	VAL	A	61	35.763	47.756	25.483	1.00	43.19
ATOM	24	C	VAL	A	61	35.243	47.069	26.738	1.00	41.81
ATOM	25	O	VAL	A	61	35.876	46.099	27.247	1.00	42.54
ATOM	26	CB	VAL	A	61	36.532	49.035	25.895	1.00	43.62
ATOM	27	CG1	VAL	A	61	37.069	49.730	24.655	1.00	44.38
ATOM	28	CG2	VAL	A	61	35.621	49.975	26.676	1.00	44.28
ATOM	29	N	GLU	A	62	34.114	47.542	27.252	1.00	40.86
ATOM	30	CA	GLU	A	62	33.517	46.959	28.470	1.00	40.02
ATOM	31	C	GLU	A	62	33.208	45.473	28.320	1.00	36.45
ATOM	32	O	GLU	A	62	33.366	44.685	29.301	1.00	36.49
ATOM	33	CB	GLU	A	62	32.226	47.700	28.832	1.00	43.76
ATOM	34	CG	GLU	A	62	32.399	48.895	29.764	1.00	48.74
ATOM	35	CD	GLU	A	62	32.743	48.486	31.188	1.00	51.91
ATOM	36	OE1	GLU	A	62	32.317	47.387	31.612	1.00	53.41
ATOM	37	OE2	GLU	A	62	33.423	49.271	31.890	1.00	53.64
ATOM	38	N	MET	A	63	32.780	45.062	27.129	1.00	30.86
ATOM	39	CA	MET	A	63	32.421	43.643	26.896	1.00	27.79
ATOM	40	C	MET	A	63	33.491	42.741	26.279	1.00	26.02
ATOM	41	O	MET	A	63	33.354	41.476	26.310	1.00	25.25
ATOM	42	CB	MET	A	63	31.130	43.578	26.078	1.00	25.63
ATOM	43	CG	MET	A	63	29.942	44.133	26.858	1.00	24.89
ATOM	44	SD	MET	A	63	28.392	44.180	25.960	1.00	23.85
ATOM	45	CE	MET	A	63	28.431	45.848	25.316	1.00	24.18
ATOM	46	N	VAL	A	64	34.551	43.330	25.736	1.00	23.39
ATOM	47	CA	VAL	A	64	35.639	42.516	25.143	1.00	20.76
ATOM	48	C	VAL	A	64	36.263	41.634	26.216	1.00	20.06
ATOM	49	O	VAL	A	64	36.531	42.095	27.370	1.00	18.87
ATOM	50	CB	VAL	A	64	36.740	43.407	24.517	1.00	21.16
ATOM	51	CG1	VAL	A	64	37.958	42.567	24.151	1.00	18.99
ATOM	52	CG2	VAL	A	64	36.193	44.092	23.266	1.00	21.01
ATOM	53	N	ASP	A	65	36.487	40.373	25.869	1.00	18.21
ATOM	54	CA	ASP	A	65	37.091	39.397	26.800	1.00	18.56
ATOM	55	C	ASP	A	65	36.280	39.174	28.071	1.00	17.80
ATOM	56	O	ASP	A	65	36.869	38.964	29.165	1.00	16.29
ATOM	57	CB	ASP	A	65	38.508	39.829	27.194	1.00	21.53
ATOM	58	CG	ASP	A	65	39.409	40.055	25.993	1.00	22.65

ATOM	59	OD1	ASP	A	65	39.162	39.451	24.930	1.00	23.75
ATOM	60	OD2	ASP	A	65	40.375	40.831	26.117	1.00	24.72
ATOM	61	N	ASN	A	66	34.955	39.209	27.969	1.00	16.59
ATOM	62	CA	ASN	A	66	34.090	38.987	29.156	1.00	16.58
ATOM	63	C	ASN	A	66	33.719	37.508	29.274	1.00	17.20
ATOM	64	O	ASN	A	66	32.815	37.125	30.070	1.00	19.23
ATOM	65	CB	ASN	A	66	32.817	39.845	29.059	1.00	14.62
ATOM	66	CG	ASN	A	66	31.967	39.516	27.835	1.00	15.57
ATOM	67	OD1	ASN	A	66	32.381	38.714	26.937	1.00	16.31
ATOM	68	ND2	ASN	A	66	30.788	40.120	27.760	1.00	14.85
ATOM	69	N	LEU	A	67	34.409	36.664	28.515	1.00	17.73
ATOM	70	CA	LEU	A	67	34.134	35.206	28.529	1.00	17.36
ATOM	71	C	LEU	A	67	35.295	34.328	28.985	1.00	16.04
ATOM	72	O	LEU	A	67	36.499	34.701	28.842	1.00	16.38
ATOM	73	CB	LEU	A	67	33.707	34.757	27.128	1.00	17.19
ATOM	74	CG	LEU	A	67	32.226	34.504	26.839	1.00	18.63
ATOM	75	CD1	LEU	A	67	31.349	35.604	27.407	1.00	16.94
ATOM	76	CD2	LEU	A	67	32.049	34.375	25.330	1.00	18.67
ATOM	77	N	ARG	A	68	34.956	33.166	29.531	1.00	14.58
ATOM	78	CA	ARG	A	68	35.961	32.173	29.973	1.00	16.73
ATOM	79	C	ARG	A	68	35.394	30.775	29.717	1.00	15.78
ATOM	80	O	ARG	A	68	34.154	30.610	29.500	1.00	13.85
ATOM	81	CB	ARG	A	68	36.299	32.349	31.459	1.00	18.19
ATOM	82	CG	ARG	A	68	37.086	33.623	31.766	1.00	21.67
ATOM	83	CD	ARG	A	68	37.571	33.646	33.213	1.00	23.25
ATOM	84	NE	ARG	A	68	36.462	33.653	34.165	1.00	26.34
ATOM	85	CZ	ARG	A	68	36.598	33.500	35.482	1.00	27.29
ATOM	86	NH1	ARG	A	68	37.802	33.324	36.015	1.00	25.91
ATOM	87	NH2	ARG	A	68	35.530	33.527	36.271	1.00	26.77
ATOM	88	N	GLY	A	69	36.262	29.769	29.726	1.00	14.89
ATOM	89	CA	GLY	A	69	35.816	28.409	29.486	1.00	15.62
ATOM	90	C	GLY	A	69	36.505	27.806	28.277	1.00	16.66
ATOM	91	O	GLY	A	69	37.526	28.367	27.771	1.00	15.60
ATOM	92	N	LYS	A	70	35.989	26.676	27.804	1.00	17.25
ATOM	93	CA	LYS	A	70	36.556	25.973	26.629	1.00	16.95
ATOM	94	C	LYS	A	70	35.472	25.138	25.949	1.00	16.87
ATOM	95	O	LYS	A	70	34.394	24.864	26.562	1.00	17.19
ATOM	96	CB	LYS	A	70	37.737	25.092	27.058	1.00	18.62
ATOM	97	CG	LYS	A	70	37.518	24.303	28.348	1.00	19.97
ATOM	98	CD	LYS	A	70	38.737	23.446	28.667	1.00	22.43
ATOM	99	CE	LYS	A	70	38.538	22.611	29.926	1.00	23.77
ATOM	100	NZ	LYS	A	70	39.660	21.638	30.129	1.00	22.43
ATOM	101	N	SER	A	71	35.714	24.729	24.706	1.00	15.11
ATOM	102	CA	SER	A	71	34.706	23.950	23.940	1.00	14.34
ATOM	103	C	SER	A	71	34.155	22.730	24.667	1.00	14.36
ATOM	104	O	SER	A	71	32.918	22.446	24.600	1.00	13.81
ATOM	105	CB	SER	A	71	35.281	23.523	22.581	1.00	14.97
ATOM	106	OG	SER	A	71	36.456	22.743	22.732	1.00	15.41
ATOM	107	N	GLY	A	72	35.024	22.005	25.362	1.00	14.38
ATOM	108	CA	GLY	A	72	34.588	20.815	26.072	1.00	14.63
ATOM	109	C	GLY	A	72	33.661	21.022	27.262	1.00	16.49
ATOM	110	O	GLY	A	72	32.772	20.159	27.537	1.00	16.20
ATOM	111	N	GLN	A	73	33.814	22.129	27.979	1.00	16.78
ATOM	112	CA	GLN	A	73	32.965	22.369	29.167	1.00	18.67
ATOM	113	C	GLN	A	73	32.040	23.570	29.038	1.00	18.70
ATOM	114	O	GLN	A	73	31.223	23.858	29.967	1.00	19.81
ATOM	115	CB	GLN	A	73	33.852	22.522	30.401	1.00	20.09
ATOM	116	CG	GLN	A	73	34.924	21.433	30.493	1.00	24.21
ATOM	117	CD	GLN	A	73	35.624	21.400	31.837	1.00	24.83
ATOM	118	OE1	GLN	A	73	36.048	22.467	32.380	1.00	26.53
ATOM	119	NE2	GLN	A	73	35.769	20.206	32.395	1.00	25.73
ATOM	120	N	GLY	A	74	32.138	24.274	27.914	1.00	17.65

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ATOM    121  CA  GLY A  74      31.292  25.429  27.688  1.00 15.83
ATOM    122  C   GLY A  74      31.939  26.746  28.068  1.00 15.56
ATOM    123  O   GLY A  74      32.837  26.799  28.962  1.00 17.53
ATOM    124  N   TYR A  75      31.517  27.814  27.403  1.00 13.96
ATOM    125  CA  TYR A  75      32.041  29.164  27.686  1.00 16.12
ATOM    126  C   TYR A  75      30.991  29.903  28.502  1.00 14.92
ATOM    127  O   TYR A  75      29.758  29.793  28.217  1.00 14.71
ATOM    128  CB  TYR A  75      32.324  29.918  26.385  1.00 17.79
ATOM    129  CG  TYR A  75      33.490  29.354  25.605  1.00 18.92
ATOM    130  CD1 TYR A  75      33.326  28.271  24.742  1.00 19.83
ATOM    131  CD2 TYR A  75      34.763  29.909  25.735  1.00 20.43
ATOM    132  CE1 TYR A  75      34.409  27.757  24.020  1.00 21.98
ATOM    133  CE2 TYR A  75      35.847  29.407  25.025  1.00 21.04
ATOM    134  CZ  TYR A  75      35.666  28.339  24.170  1.00 22.04
ATOM    135  OH  TYR A  75      36.746  27.882  23.456  1.00 22.86
ATOM    136  N   TYR A  76      31.432  30.653  29.507  1.00 13.66
ATOM    137  CA  TYR A  76      30.478  31.360  30.368  1.00 12.95
ATOM    138  C   TYR A  76      30.753  32.837  30.593  1.00 13.47
ATOM    139  O   TYR A  76      31.901  33.345  30.391  1.00 13.77
ATOM    140  CB  TYR A  76      30.395  30.662  31.725  1.00 13.31
ATOM    141  CG  TYR A  76      31.723  30.548  32.446  1.00 14.55
ATOM    142  CD1 TYR A  76      32.601  29.497  32.174  1.00 16.16
ATOM    143  CD2 TYR A  76      32.105  31.495  33.392  1.00 15.68
ATOM    144  CE1 TYR A  76      33.829  29.392  32.832  1.00 17.64
ATOM    145  CE2 TYR A  76      33.329  31.402  34.055  1.00 18.14
ATOM    146  CZ  TYR A  76      34.183  30.348  33.770  1.00 18.24
ATOM    147  OH  TYR A  76      35.390  30.252  34.428  1.00 21.79
ATOM    148  N   VAL A  77      29.716  33.546  31.017  1.00 12.55
ATOM    149  CA  VAL A  77      29.844  34.980  31.298  1.00 14.17
ATOM    150  C   VAL A  77      29.390  35.225  32.727  1.00 15.16
ATOM    151  O   VAL A  77      28.564  34.439  33.283  1.00 16.09
ATOM    152  CB  VAL A  77      28.975  35.821  30.336  1.00 13.43
ATOM    153  CG1 VAL A  77      27.495  35.528  30.567  1.00 11.59
ATOM    154  CG2 VAL A  77      29.281  37.305  30.524  1.00 10.74
ATOM    155  N   GLU A  78      29.905  36.276  33.352  1.00 16.88
ATOM    156  CA  GLU A  78      29.486  36.571  34.731  1.00 17.45
ATOM    157  C   GLU A  78      28.178  37.345  34.706  1.00 16.89
ATOM    158  O   GLU A  78      27.961  38.239  33.826  1.00 14.65
ATOM    159  CB  GLU A  78      30.538  37.392  35.479  1.00 19.11
ATOM    160  CG  GLU A  78      30.222  37.503  36.974  1.00 24.70
ATOM    161  CD  GLU A  78      31.225  38.342  37.757  1.00 26.24
ATOM    162  OE1 GLU A  78      31.162  39.584  37.679  1.00 27.53
ATOM    163  OE2 GLU A  78      32.076  37.755  38.452  1.00 29.49
ATOM    164  N   MET A  79      27.296  37.012  35.641  1.00 16.65
ATOM    165  CA  MET A  79      25.992  37.684  35.761  1.00 17.22
ATOM    166  C   MET A  79      25.610  37.768  37.232  1.00 17.77
ATOM    167  O   MET A  79      26.208  37.066  38.100  1.00 18.29
ATOM    168  CB  MET A  79      24.908  36.899  35.007  1.00 16.88
ATOM    169  CG  MET A  79      25.070  36.874  33.492  1.00 16.65
ATOM    170  SD  MET A  79      23.798  35.865  32.673  1.00 17.43
ATOM    171  CE  MET A  79      22.442  37.003  32.577  1.00 15.55
ATOM    172  N   THR A  80      24.637  38.617  37.539  1.00 17.73
ATOM    173  CA  THR A  80      24.146  38.741  38.917  1.00 17.50
ATOM    174  C   THR A  80      22.632  38.630  38.853  1.00 17.85
ATOM    175  O   THR A  80      21.995  39.075  37.851  1.00 17.14
ATOM    176  CB  THR A  80      24.524  40.100  39.550  1.00 18.12
ATOM    177  OG1 THR A  80      23.851  41.158  38.857  1.00 18.55
ATOM    178  CG2 THR A  80      26.031  40.328  39.474  1.00 16.48
ATOM    179  N   VAL A  81      22.042  38.020  39.874  1.00 18.24
ATOM    180  CA  VAL A  81      20.573  37.882  39.959  1.00 20.23
ATOM    181  C   VAL A  81      20.145  38.274  41.375  1.00 21.18
ATOM    182  O   VAL A  81      20.929  38.093  42.362  1.00 20.31
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ATOM    183  CB  VAL A  81      20.105  36.429  39.700  1.00 20.43
ATOM    184  CG1 VAL A  81      20.566  35.959  38.334  1.00 21.49
ATOM    185  CG2 VAL A  81      20.639  35.518  40.777  1.00 21.78
ATOM    186  N   GLY A  82      18.938  38.817  41.497  1.00 21.84
ATOM    187  CA  GLY A  82      18.421  39.200  42.799  1.00 21.10
ATOM    188  C   GLY A  82      18.973  40.475  43.404  1.00 21.47
ATOM    189  O   GLY A  82      19.864  41.159  42.814  1.00 21.97
ATOM    190  N   SER A  83      18.454  40.808  44.581  1.00 22.27
ATOM    191  CA  SER A  83      18.869  42.012  45.335  1.00 22.02
ATOM    192  C   SER A  83      18.996  41.607  46.795  1.00 20.16
ATOM    193  O   SER A  83      18.002  41.120  47.410  1.00 20.07
ATOM    194  CB  SER A  83      17.804  43.104  45.213  1.00 21.98
ATOM    195  OG  SER A  83      17.356  43.229  43.874  1.00 23.70
ATOM    196  N   PRO A  84      20.198  41.734  47.380  1.00 21.14
ATOM    197  CA  PRO A  84      21.454  42.221  46.785  1.00 20.45
ATOM    198  C   PRO A  84      21.911  41.288  45.656  1.00 20.37
ATOM    199  O   PRO A  84      21.508  40.086  45.606  1.00 18.46
ATOM    200  CB  PRO A  84      22.434  42.193  47.962  1.00 19.74
ATOM    201  CG  PRO A  84      21.548  42.320  49.166  1.00 20.71
ATOM    202  CD  PRO A  84      20.377  41.447  48.815  1.00 19.44
ATOM    203  N   PRO A  85      22.754  41.790  44.741  1.00 20.53
ATOM    204  CA  PRO A  85      23.258  40.997  43.616  1.00 20.58
ATOM    205  C   PRO A  85      23.949  39.706  44.046  1.00 20.81
ATOM    206  O   PRO A  85      24.854  39.720  44.936  1.00 21.15
ATOM    207  CB  PRO A  85      24.240  41.947  42.932  1.00 20.87
ATOM    208  CG  PRO A  85      23.732  43.294  43.282  1.00 22.23
ATOM    209  CD  PRO A  85      23.340  43.141  44.724  1.00 21.41
ATOM    210  N   GLN A  86      23.541  38.590  43.453  1.00 20.05
ATOM    211  CA  GLN A  86      24.174  37.289  43.752  1.00 19.63
ATOM    212  C   GLN A  86      24.904  36.923  42.472  1.00 20.50
ATOM    213  O   GLN A  86      24.263  36.622  41.412  1.00 19.85
ATOM    214  CB  GLN A  86      23.127  36.227  44.097  1.00 19.82
ATOM    215  CG  GLN A  86      22.283  36.586  45.314  1.00 18.97
ATOM    216  CD  GLN A  86      21.292  35.506  45.693  1.00 19.84
ATOM    217  OE1 GLN A  86      20.226  35.801  46.316  1.00 21.21
ATOM    218  NE2 GLN A  86      21.603  34.259  45.354  1.00 17.54
ATOM    219  N   THR A  87      26.229  36.969  42.527  1.00 19.61
ATOM    220  CA  THR A  87      27.057  36.669  41.346  1.00 19.61
ATOM    221  C   THR A  87      27.088  35.188  40.994  1.00 18.63
ATOM    222  O   THR A  87      27.220  34.302  41.892  1.00 18.56
ATOM    223  CB  THR A  87      28.501  37.164  41.549  1.00 19.88
ATOM    224  OG1 THR A  87      28.486  38.558  41.887  1.00 20.57
ATOM    225  CG2 THR A  87      29.304  36.977  40.278  1.00 18.65
ATOM    226  N   LEU A  88      26.972  34.907  39.701  1.00 18.38
ATOM    227  CA  LEU A  88      26.991  33.522  39.193  1.00 18.18
ATOM    228  C   LEU A  88      27.572  33.496  37.781  1.00 18.11
ATOM    229  O   LEU A  88      27.353  34.457  36.974  1.00 18.86
ATOM    230  CB  LEU A  88      25.568  32.952  39.159  1.00 16.21
ATOM    231  CG  LEU A  88      24.825  32.828  40.495  1.00 18.20
ATOM    232  CD1 LEU A  88      23.366  32.474  40.226  1.00 18.10
ATOM    233  CD2 LEU A  88      25.484  31.766  41.379  1.00 16.56
ATOM    234  N   ASN A  89      28.317  32.443  37.459  1.00 15.84
ATOM    235  CA  ASN A  89      28.876  32.312  36.101  1.00 16.22
ATOM    236  C   ASN A  89      27.841  31.544  35.300  1.00 16.03
ATOM    237  O   ASN A  89      27.363  30.450  35.735  1.00 15.05
ATOM    238  CB  ASN A  89      30.208  31.565  36.114  1.00 15.71
ATOM    239  CG  ASN A  89      31.324  32.396  36.700  1.00 16.10
ATOM    240  OD1 ASN A  89      31.390  33.650  36.477  1.00 15.48
ATOM    241  ND2 ASN A  89      32.217  31.750  37.439  1.00 14.07
ATOM    242  N   ILE A  90      27.485  32.091  34.145  1.00 15.55
ATOM    243  CA  ILE A  90      26.445  31.494  33.292  1.00 14.59
ATOM    244  C   ILE A  90      26.960  31.052  31.930  1.00 15.07
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ATOM    245  O   ILE A  90      27.578  31.867  31.173  1.00 13.01
ATOM    246  CB  ILE A  90      25.301  32.512  33.084  1.00 14.44
ATOM    247  CG1 ILE A  90      24.884  33.098  34.437  1.00 14.15
ATOM    248  CG2 ILE A  90      24.114  31.847  32.407  1.00 14.29
ATOM    249  CD1 ILE A  90      24.356  32.062  35.426  1.00 13.44
ATOM    250  N   LEU A  91      26.714  29.790  31.590  1.00 15.08
ATOM    251  CA  LEU A  91      27.153  29.249  30.284  1.00 15.63
ATOM    252  C   LEU A  91      26.313  29.878  29.174  1.00 16.04
ATOM    253  O   LEU A  91      25.041  29.904  29.250  1.00 16.72
ATOM    254  CB  LEU A  91      27.008  27.721  30.265  1.00 14.67
ATOM    255  CG  LEU A  91      27.450  26.945  29.012  1.00 15.49
ATOM    256  CD1 LEU A  91      27.692  25.485  29.364  1.00 15.10
ATOM    257  CD2 LEU A  91      26.393  27.052  27.925  1.00 15.54
ATOM    258  N   VAL A  92      26.995  30.408  28.164  1.00 16.13
ATOM    259  CA  VAL A  92      26.336  31.051  27.003  1.00 15.39
ATOM    260  C   VAL A  92      25.901  29.960  26.038  1.00 15.51
ATOM    261  O   VAL A  92      26.761  29.243  25.440  1.00 16.92
ATOM    262  CB  VAL A  92      27.306  32.008  26.278  1.00 15.40
ATOM    263  CG1 VAL A  92      26.668  32.523  24.994  1.00 16.99
ATOM    264  CG2 VAL A  92      27.671  33.172  27.200  1.00 13.64
ATOM    265  N   ASP A  93      24.594  29.824  25.845  1.00 16.41
ATOM    266  CA  ASP A  93      24.069  28.762  24.974  1.00 14.41
ATOM    267  C   ASP A  93      23.090  29.226  23.903  1.00 15.40
ATOM    268  O   ASP A  93      21.889  29.494  24.206  1.00 15.81
ATOM    269  CB  ASP A  93      23.411  27.701  25.861  1.00 16.00
ATOM    270  CG  ASP A  93      22.897  26.512  25.078  1.00 16.45
ATOM    271  OD1 ASP A  93      23.536  26.133  24.076  1.00 17.23
ATOM    272  OD2 ASP A  93      21.863  25.938  25.481  1.00 16.68
ATOM    273  N   THR A  94      23.550  29.326  22.657  1.00 13.38
ATOM    274  CA  THR A  94      22.636  29.745  21.574  1.00 13.70
ATOM    275  C   THR A  94      21.811  28.549  21.109  1.00 13.68
ATOM    276  O   THR A  94      20.941  28.671  20.190  1.00 14.18
ATOM    277  CB  THR A  94      23.397  30.349  20.362  1.00 14.99
ATOM    278  OG1 THR A  94      24.279  29.370  19.798  1.00 14.96
ATOM    279  CG2 THR A  94      24.201  31.568  20.794  1.00 14.04
ATOM    280  N   GLY A  95      22.053  27.392  21.719  1.00 14.90
ATOM    281  CA  GLY A  95      21.309  26.199  21.351  1.00 15.51
ATOM    282  C   GLY A  95      20.108  25.969  22.255  1.00 16.96
ATOM    283  O   GLY A  95      19.516  24.850  22.275  1.00 16.90
ATOM    284  N   SER A  96      19.721  26.987  23.011  1.00 17.38
ATOM    285  CA  SER A  96      18.562  26.851  23.922  1.00 17.95
ATOM    286  C   SER A  96      17.990  28.231  24.226  1.00 17.07
ATOM    287  O   SER A  96      18.573  29.269  23.803  1.00 14.94
ATOM    288  CB  SER A  96      19.005  26.174  25.219  1.00 18.55
ATOM    289  OG  SER A  96      19.640  26.894  26.276  1.00 26.99
ATOM    290  N   SER A  97      16.869  28.292  24.936  1.00 16.25
ATOM    291  CA  SER A  97      16.290  29.614  25.258  1.00 18.39
ATOM    292  C   SER A  97      15.740  29.776  26.670  1.00 17.83
ATOM    293  O   SER A  97      14.866  30.653  26.932  1.00 18.75
ATOM    294  CB  SER A  97      15.224  29.993  24.227  1.00 18.88
ATOM    295  OG  SER A  97      14.633  28.850  23.651  1.00 23.68
ATOM    296  N   ASN A  98      16.229  28.959  27.592  1.00 17.57
ATOM    297  CA  ASN A  98      15.809  29.073  28.993  1.00 16.01
ATOM    298  C   ASN A  98      16.963  29.611  29.821  1.00 16.51
ATOM    299  O   ASN A  98      18.127  29.109  29.709  1.00 16.69
ATOM    300  CB  ASN A  98      15.401  27.720  29.566  1.00 13.74
ATOM    301  CG  ASN A  98      13.969  27.359  29.241  1.00 16.04
ATOM    302  OD1 ASN A  98      13.669  26.795  28.139  1.00 13.27
ATOM    303  ND2 ASN A  98      13.058  27.680  30.158  1.00 13.26
ATOM    304  N   PHE A  99      16.688  30.640  30.614  1.00 14.45
ATOM    305  CA  PHE A  99      17.710  31.196  31.519  1.00 13.19
ATOM    306  C   PHE A  99      17.453  30.424  32.812  1.00 13.23
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ATOM    307  O   PHE A  99      16.319  30.466  33.384  1.00 11.00
ATOM    308  CB  PHE A  99      17.491  32.699  31.722  1.00 13.54
ATOM    309  CG  PHE A  99      18.390  33.318  32.761  1.00 14.79
ATOM    310  CD1 PHE A  99      19.741  32.978  32.836  1.00 15.02
ATOM    311  CD2 PHE A  99      17.889  34.258  33.657  1.00 16.17
ATOM    312  CE1 PHE A  99      20.576  33.564  33.784  1.00 14.99
ATOM    313  CE2 PHE A  99      18.718  34.852  34.610  1.00 16.36
ATOM    314  CZ  PHE A  99      20.064  34.503  34.674  1.00 14.33
ATOM    315  N   ALA A 100      18.457  29.691  33.274  1.00 11.83
ATOM    316  CA  ALA A 100      18.298  28.889  34.497  1.00 12.34
ATOM    317  C   ALA A 100      19.594  28.836  35.277  1.00 14.53
ATOM    318  O   ALA A 100      20.722  28.896  34.684  1.00 15.19
ATOM    319  CB  ALA A 100      17.849  27.486  34.138  1.00 13.09
ATOM    320  N   VAL A 101      19.467  28.727  36.595  1.00 13.51
ATOM    321  CA  VAL A 101      20.640  28.686  37.473  1.00 13.80
ATOM    322  C   VAL A 101      20.429  27.693  38.610  1.00 15.86
ATOM    323  O   VAL A 101      19.253  27.424  39.031  1.00 13.90
ATOM    324  CB  VAL A 101      20.912  30.082  38.075  1.00 14.68
ATOM    325  CG1 VAL A 101      21.126  31.098  36.962  1.00 12.49
ATOM    326  CG2 VAL A 101      19.743  30.509  38.953  1.00 13.11
ATOM    327  N   GLY A 102      21.528  27.120  39.098  1.00 16.51
ATOM    328  CA  GLY A 102      21.437  26.189  40.207  1.00 17.46
ATOM    329  C   GLY A 102      20.858  26.966  41.375  1.00 19.61
ATOM    330  O   GLY A 102      21.303  28.128  41.641  1.00 19.12
ATOM    331  N   ALA A 103      19.875  26.395  42.065  1.00 19.81
ATOM    332  CA  ALA A 103      19.241  27.092  43.212  1.00 22.41
ATOM    333  C   ALA A 103      19.098  26.169  44.414  1.00 23.71
ATOM    334  O   ALA A 103      18.196  26.366  45.293  1.00 24.50
ATOM    335  CB  ALA A 103      17.880  27.627  42.807  1.00 21.12
ATOM    336  N   ALA A 104      19.967  25.168  44.470  1.00 23.53
ATOM    337  CA  ALA A 104      19.979  24.180  45.566  1.00 24.47
ATOM    338  C   ALA A 104      21.341  23.505  45.517  1.00 24.98
ATOM    339  O   ALA A 104      21.974  23.413  44.419  1.00 26.65
ATOM    340  CB  ALA A 104      18.869  23.150  45.367  1.00 23.55
ATOM    341  N   PRO A 105      21.836  23.026  46.668  1.00 25.27
ATOM    342  CA  PRO A 105      23.140  22.361  46.733  1.00 24.87
ATOM    343  C   PRO A 105      23.328  21.286  45.672  1.00 24.16
ATOM    344  O   PRO A 105      22.350  20.594  45.251  1.00 24.35
ATOM    345  CB  PRO A 105      23.159  21.778  48.143  1.00 25.36
ATOM    346  CG  PRO A 105      22.347  22.763  48.920  1.00 25.71
ATOM    347  CD  PRO A 105      21.183  23.020  47.990  1.00 25.99
ATOM    348  N   HIS A 106      24.566  21.135  45.227  1.00 24.93
ATOM    349  CA  HIS A 106      24.918  20.119  44.223  1.00 23.63
ATOM    350  C   HIS A 106      26.402  19.843  44.367  1.00 24.29
ATOM    351  O   HIS A 106      27.207  20.790  44.596  1.00 24.19
ATOM    352  CB  HIS A 106      24.646  20.622  42.807  1.00 24.15
ATOM    353  CG  HIS A 106      24.887  19.587  41.756  1.00 24.43
ATOM    354  ND1 HIS A 106      23.912  18.702  41.348  1.00 25.53
ATOM    355  CD2 HIS A 106      26.012  19.244  41.084  1.00 23.79
ATOM    356  CE1 HIS A 106      24.426  17.857  40.471  1.00 25.66
ATOM    357  NE2 HIS A 106      25.699  18.164  40.294  1.00 24.92
ATOM    358  N   PRO A 107      26.811  18.572  44.236  1.00 25.36
ATOM    359  CA  PRO A 107      28.224  18.200  44.358  1.00 26.23
ATOM    360  C   PRO A 107      29.164  19.025  43.474  1.00 26.26
ATOM    361  O   PRO A 107      30.335  19.296  43.866  1.00 28.01
ATOM    362  CB  PRO A 107      28.225  16.722  43.972  1.00 26.21
ATOM    363  CG  PRO A 107      26.875  16.259  44.418  1.00 26.75
ATOM    364  CD  PRO A 107      25.977  17.384  43.971  1.00 25.04
ATOM    365  N   PHE A 108      28.695  19.435  42.299  1.00 25.94
ATOM    366  CA  PHE A 108      29.556  20.218  41.384  1.00 26.76
ATOM    367  C   PHE A 108      29.358  21.726  41.450  1.00 26.66
ATOM    368  O   PHE A 108      30.103  22.494  40.778  1.00 26.81
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ATOM	369	CB	PHE	A	108	29.368	19.754	39.936	1.00	26.67
ATOM	370	CG	PHE	A	108	29.665	18.300	39.720	1.00	26.80
ATOM	371	CD1	PHE	A	108	30.531	17.614	40.569	1.00	27.67
ATOM	372	CD2	PHE	A	108	29.090	17.615	38.655	1.00	27.12
ATOM	373	CE1	PHE	A	108	30.819	16.262	40.359	1.00	27.99
ATOM	374	CE2	PHE	A	108	29.369	16.267	38.433	1.00	26.65
ATOM	375	CZ	PHE	A	108	30.235	15.587	39.286	1.00	26.94
ATOM	376	N	LEU	A	109	28.386	22.180	42.231	1.00	26.14
ATOM	377	CA	LEU	A	109	28.144	23.629	42.346	1.00	27.17
ATOM	378	C	LEU	A	109	28.914	24.248	43.510	1.00	29.20
ATOM	379	O	LEU	A	109	28.861	23.743	44.669	1.00	26.91
ATOM	380	CB	LEU	A	109	26.647	23.911	42.498	1.00	25.73
ATOM	381	CG	LEU	A	109	25.811	23.714	41.230	1.00	25.94
ATOM	382	CD1	LEU	A	109	24.343	23.983	41.530	1.00	24.99
ATOM	383	CD2	LEU	A	109	26.310	24.657	40.136	1.00	24.26
ATOM	384	N	HIS	A	110	29.632	25.328	43.213	1.00	32.94
ATOM	385	CA	HIS	A	110	30.442	26.077	44.207	1.00	35.82
ATOM	386	C	HIS	A	110	29.533	27.015	44.983	1.00	33.93
ATOM	387	O	HIS	A	110	29.732	27.265	46.209	1.00	34.20
ATOM	388	CB	HIS	A	110	31.501	26.915	43.485	1.00	42.49
ATOM	389	CG	HIS	A	110	32.907	26.469	43.732	1.00	47.84
ATOM	390	ND1	HIS	A	110	33.509	26.558	44.969	1.00	50.74
ATOM	391	CD2	HIS	A	110	33.834	25.934	42.899	1.00	49.74
ATOM	392	CE1	HIS	A	110	34.746	26.098	44.888	1.00	51.83
ATOM	393	NE2	HIS	A	110	34.968	25.713	43.644	1.00	51.38
ATOM	394	N	ARG	A	111	28.547	27.553	44.279	1.00	31.13
ATOM	395	CA	ARG	A	111	27.579	28.494	44.857	1.00	28.72
ATOM	396	C	ARG	A	111	26.287	28.331	44.072	1.00	28.16
ATOM	397	O	ARG	A	111	26.267	27.652	43.000	1.00	27.40
ATOM	398	CB	ARG	A	111	28.108	29.924	44.717	1.00	28.09
ATOM	399	CG	ARG	A	111	28.550	30.255	43.305	1.00	26.48
ATOM	400	CD	ARG	A	111	29.216	31.616	43.201	1.00	25.86
ATOM	401	NE	ARG	A	111	29.723	31.831	41.849	1.00	25.21
ATOM	402	CZ	ARG	A	111	30.423	32.892	41.465	1.00	24.44
ATOM	403	NH1	ARG	A	111	30.708	33.850	42.337	1.00	25.08
ATOM	404	NH2	ARG	A	111	30.828	32.995	40.205	1.00	22.62
ATOM	405	N	TYR	A	112	25.207	28.922	44.566	1.00	26.27
ATOM	406	CA	TYR	A	112	23.922	28.814	43.866	1.00	23.70
ATOM	407	C	TYR	A	112	22.955	29.916	44.250	1.00	22.77
ATOM	408	O	TYR	A	112	23.140	30.633	45.283	1.00	21.10
ATOM	409	CB	TYR	A	112	23.295	27.437	44.119	1.00	25.47
ATOM	410	CG	TYR	A	112	23.036	27.111	45.575	1.00	27.20
ATOM	411	CD1	TYR	A	112	21.885	27.569	46.222	1.00	28.51
ATOM	412	CD2	TYR	A	112	23.946	26.353	46.309	1.00	27.51
ATOM	413	CE1	TYR	A	112	21.647	27.276	47.565	1.00	27.78
ATOM	414	CE2	TYR	A	112	23.720	26.058	47.651	1.00	28.63
ATOM	415	CZ	TYR	A	112	22.570	26.522	48.270	1.00	28.98
ATOM	416	OH	TYR	A	112	22.352	26.228	49.591	1.00	30.28
ATOM	417	N	TYR	A	113	21.927	30.069	43.428	1.00	19.32
ATOM	418	CA	TYR	A	113	20.896	31.090	43.624	1.00	18.94
ATOM	419	C	TYR	A	113	20.047	30.807	44.857	1.00	17.90
ATOM	420	O	TYR	A	113	19.480	29.688	45.011	1.00	19.37
ATOM	421	CB	TYR	A	113	20.027	31.141	42.369	1.00	17.76
ATOM	422	CG	TYR	A	113	18.887	32.135	42.378	1.00	17.68
ATOM	423	CD1	TYR	A	113	19.024	33.397	42.963	1.00	16.86
ATOM	424	CD2	TYR	A	113	17.709	31.854	41.688	1.00	16.79
ATOM	425	CE1	TYR	A	113	18.020	34.349	42.848	1.00	17.05
ATOM	426	CE2	TYR	A	113	16.704	32.796	41.563	1.00	16.02
ATOM	427	CZ	TYR	A	113	16.858	34.038	42.138	1.00	17.36
ATOM	428	OH	TYR	A	113	15.848	34.963	41.984	1.00	16.62
ATOM	429	N	GLN	A	114	19.967	31.790	45.746	1.00	18.68
ATOM	430	CA	GLN	A	114	19.156	31.673	46.983	1.00	20.28

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ATOM    431  C   GLN A 114      18.057  32.719  46.897  1.00 19.59
ATOM    432  O   GLN A 114      18.285  33.933  47.192  1.00 20.34
ATOM    433  CB  GLN A 114      20.028  31.912  48.216  1.00 19.79
ATOM    434  CG  GLN A 114      21.048  30.814  48.434  1.00 22.79
ATOM    435  CD  GLN A 114      21.942  31.063  49.626  1.00 24.34
ATOM    436  OE1 GLN A 114      22.708  32.073  49.668  1.00 26.47
ATOM    437  NE2 GLN A 114      21.876  30.173  50.606  1.00 24.49
ATOM    438  N   ARG A 115      16.876  32.275  46.479  1.00 20.48
ATOM    439  CA  ARG A 115      15.703  33.159  46.305  1.00 21.24
ATOM    440  C   ARG A 115      15.234  33.837  47.583  1.00 21.94
ATOM    441  O   ARG A 115      14.784  35.022  47.546  1.00 21.40
ATOM    442  CB  ARG A 115      14.550  32.366  45.686  1.00 20.21
ATOM    443  CG  ARG A 115      14.807  31.953  44.240  1.00 20.95
ATOM    444  CD  ARG A 115      13.917  30.796  43.824  1.00 20.32
ATOM    445  NE  ARG A 115      14.305  29.567  44.508  1.00 20.45
ATOM    446  CZ  ARG A 115      13.626  28.428  44.448  1.00 19.47
ATOM    447  NH1 ARG A 115      12.514  28.352  43.732  1.00 20.02
ATOM    448  NH2 ARG A 115      14.061  27.366  45.106  1.00 21.63
ATOM    449  N   GLN A 116      15.323  33.138  48.710  1.00 22.93
ATOM    450  CA  GLN A 116      14.880  33.723  49.993  1.00 24.99
ATOM    451  C   GLN A 116      15.718  34.953  50.343  1.00 23.86
ATOM    452  O   GLN A 116      15.242  35.873  51.080  1.00 24.27
ATOM    453  CB  GLN A 116      14.972  32.691  51.123  1.00 27.81
ATOM    454  CG  GLN A 116      16.391  32.280  51.502  1.00 32.89
ATOM    455  CD  GLN A 116      16.999  31.257  50.550  1.00 36.05
ATOM    456  OE1 GLN A 116      16.955  31.423  49.295  1.00 36.88
ATOM    457  NE2 GLN A 116      17.577  30.199  51.112  1.00 37.21
ATOM    458  N   LEU A 117      16.944  35.006  49.833  1.00 20.91
ATOM    459  CA  LEU A 117      17.831  36.153  50.112  1.00 20.59
ATOM    460  C   LEU A 117      17.673  37.296  49.124  1.00 19.96
ATOM    461  O   LEU A 117      18.440  38.301  49.191  1.00 18.93
ATOM    462  CB  LEU A 117      19.296  35.707  50.128  1.00 21.68
ATOM    463  CG  LEU A 117      19.887  35.224  51.454  1.00 22.49
ATOM    464  CD1 LEU A 117      19.001  34.175  52.074  1.00 22.63
ATOM    465  CD2 LEU A 117      21.286  34.675  51.210  1.00 22.12
ATOM    466  N   SER A 118      16.714  37.183  48.210  1.00 18.14
ATOM    467  CA  SER A 118      16.484  38.252  47.208  1.00 17.08
ATOM    468  C   SER A 118      15.150  38.953  47.436  1.00 16.25
ATOM    469  O   SER A 118      14.055  38.316  47.347  1.00 16.00
ATOM    470  CB  SER A 118      16.519  37.679  45.787  1.00 15.12
ATOM    471  OG  SER A 118      16.301  38.708  44.835  1.00 16.81
ATOM    472  N   SER A 119      15.210  40.250  47.711  1.00 15.31
ATOM    473  CA  SER A 119      13.991  41.044  47.973  1.00 18.09
ATOM    474  C   SER A 119      13.169  41.307  46.714  1.00 17.35
ATOM    475  O   SER A 119      11.964  41.669  46.800  1.00 17.62
ATOM    476  CB  SER A 119      14.371  42.380  48.618  1.00 16.85
ATOM    477  OG  SER A 119      15.158  43.160  47.727  1.00 18.71
ATOM    478  N   THR A 120      13.781  41.137  45.546  1.00 18.90
ATOM    479  CA  THR A 120      13.075  41.381  44.263  1.00 17.26
ATOM    480  C   THR A 120      12.587  40.104  43.594  1.00 17.17
ATOM    481  O   THR A 120      12.004  40.139  42.466  1.00 18.70
ATOM    482  CB  THR A 120      13.980  42.143  43.283  1.00 17.78
ATOM    483  OG1 THR A 120      15.305  41.609  43.355  1.00 17.35
ATOM    484  CG2 THR A 120      14.012  43.630  43.624  1.00 17.37
ATOM    485  N   TYR A 121      12.800  38.977  44.257  1.00 18.03
ATOM    486  CA  TYR A 121      12.364  37.676  43.715  1.00 18.53
ATOM    487  C   TYR A 121      10.841  37.584  43.606  1.00 18.12
ATOM    488  O   TYR A 121      10.088  38.028  44.531  1.00 19.29
ATOM    489  CB  TYR A 121      12.878  36.547  44.607  1.00 18.32
ATOM    490  CG  TYR A 121      12.187  35.225  44.368  1.00 22.03
ATOM    491  CD1 TYR A 121      12.429  34.484  43.209  1.00 21.48
ATOM    492  CD2 TYR A 121      11.268  34.725  45.291  1.00 21.95
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ATOM    493  CE1 TYR A 121      11.776  33.280  42.977  1.00 21.33
ATOM    494  CE2 TYR A 121      10.608  33.523  45.067  1.00 22.77
ATOM    495  CZ  TYR A 121      10.867  32.807  43.908  1.00 23.35
ATOM    496  OH  TYR A 121      10.206  31.622  43.682  1.00 23.63
ATOM    497  N   ARG A 122      10.365  37.039  42.492  1.00 16.86
ATOM    498  CA  ARG A 122       8.909  36.851  42.281  1.00 16.79
ATOM    499  C   ARG A 122       8.703  35.397  41.890  1.00 17.46
ATOM    500  O   ARG A 122       9.348  34.884  40.924  1.00 17.88
ATOM    501  CB  ARG A 122       8.384  37.764  41.174  1.00 14.87
ATOM    502  CG  ARG A 122       8.335  39.230  41.548  1.00 14.83
ATOM    503  CD  ARG A 122       7.895  40.067  40.369  1.00 14.98
ATOM    504  NE  ARG A 122       7.822  41.481  40.706  1.00 16.19
ATOM    505  CZ  ARG A 122       7.546  42.442  39.833  1.00 16.67
ATOM    506  NH1 ARG A 122       7.316  42.142  38.559  1.00 15.67
ATOM    507  NH2 ARG A 122       7.505  43.704  40.233  1.00 16.38
ATOM    508  N   ASP A 123       7.836  34.720  42.628  1.00 18.52
ATOM    509  CA  ASP A 123       7.538  33.296  42.388  1.00 19.00
ATOM    510  C   ASP A 123       6.435  33.147  41.347  1.00 19.87
ATOM    511  O   ASP A 123       5.342  33.757  41.490  1.00 17.59
ATOM    512  CB  ASP A 123       7.090  32.657  43.702  1.00 19.80
ATOM    513  CG  ASP A 123       6.841  31.171  43.582  1.00 20.76
ATOM    514  OD1 ASP A 123       6.933  30.615  42.463  1.00 20.41
ATOM    515  OD2 ASP A 123       6.549  30.559  44.629  1.00 22.50
ATOM    516  N   LEU A 124       6.689  32.359  40.305  1.00 20.70
ATOM    517  CA  LEU A 124       5.672  32.139  39.255  1.00 21.20
ATOM    518  C   LEU A 124       4.790  30.929  39.562  1.00 21.64
ATOM    519  O   LEU A 124       3.832  30.601  38.786  1.00 21.17
ATOM    520  CB  LEU A 124       6.343  31.978  37.888  1.00 21.51
ATOM    521  CG  LEU A 124       6.850  33.288  37.270  1.00 22.05
ATOM    522  CD1 LEU A 124       7.617  32.994  35.997  1.00 22.23
ATOM    523  CD2 LEU A 124       5.678  34.217  36.983  1.00 21.49
ATOM    524  N   ARG A 125       5.083  30.252  40.666  1.00 22.67
ATOM    525  CA  ARG A 125       4.286  29.078  41.085  1.00 25.58
ATOM    526  C   ARG A 125       4.106  28.081  39.944  1.00 26.39
ATOM    527  O   ARG A 125       2.974  27.552  39.719  1.00 26.83
ATOM    528  CB  ARG A 125       2.918  29.553  41.593  1.00 26.62
ATOM    529  CG  ARG A 125       3.016  30.511  42.783  1.00 30.02
ATOM    530  CD  ARG A 125       1.733  31.311  43.002  1.00 32.48
ATOM    531  NE  ARG A 125       1.910  32.334  44.034  1.00 36.63
ATOM    532  CZ  ARG A 125       1.049  33.323  44.282  1.00 38.12
ATOM    533  NH1 ARG A 125      -0.070  33.441  43.575  1.00 37.55
ATOM    534  NH2 ARG A 125       1.307  34.202  45.240  1.00 38.11
ATOM    535  N   LYS A 126       5.189  27.810  39.221  1.00 26.62
ATOM    536  CA  LYS A 126       5.162  26.861  38.079  1.00 26.41
ATOM    537  C   LYS A 126       6.453  26.063  37.986  1.00 24.61
ATOM    538  O   LYS A 126       7.577  26.624  38.141  1.00 22.46
ATOM    539  CB  LYS A 126       4.971  27.605  36.756  1.00 28.55
ATOM    540  CG  LYS A 126       3.539  27.804  36.326  1.00 32.76
ATOM    541  CD  LYS A 126       3.486  28.380  34.917  1.00 36.53
ATOM    542  CE  LYS A 126       2.048  28.607  34.456  1.00 38.52
ATOM    543  NZ  LYS A 126       1.234  27.355  34.550  1.00 40.78
ATOM    544  N   GLY A 127       6.326  24.770  37.731  1.00 23.25
ATOM    545  CA  GLY A 127       7.504  23.941  37.598  1.00 22.82
ATOM    546  C   GLY A 127       7.970  23.995  36.157  1.00 22.77
ATOM    547  O   GLY A 127       7.220  24.487  35.252  1.00 22.00
ATOM    548  N   VAL A 128       9.184  23.521  35.909  1.00 21.58
ATOM    549  CA  VAL A 128       9.731  23.511  34.541  1.00 22.39
ATOM    550  C   VAL A 128      10.736  22.388  34.390  1.00 21.31
ATOM    551  O   VAL A 128      11.547  22.101  35.323  1.00 21.59
ATOM    552  CB  VAL A 128      10.416  24.851  34.180  1.00 21.77
ATOM    553  CG1 VAL A 128      11.572  25.120  35.122  1.00 22.15
ATOM    554  CG2 VAL A 128      10.903  24.809  32.740  1.00 23.66
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ATOM    555  N   TYR A 129      10.700  21.744  33.233  1.00 21.64
ATOM    556  CA  TYR A 129      11.598  20.624  32.933  1.00 21.55
ATOM    557  C   TYR A 129      12.298  20.882  31.609  1.00 20.25
ATOM    558  O   TYR A 129      11.635  21.188  30.573  1.00 20.01
ATOM    559  CB  TYR A 129      10.785  19.333  32.841  1.00 23.37
ATOM    560  CG  TYR A 129      11.545  18.164  32.271  1.00 26.64
ATOM    561  CD1 TYR A 129      12.628  17.613  32.956  1.00 27.70
ATOM    562  CD2 TYR A 129      11.178  17.598  31.048  1.00 27.27
ATOM    563  CE1 TYR A 129      13.323  16.529  32.443  1.00 29.33
ATOM    564  CE2 TYR A 129      11.872  16.507  30.524  1.00 28.75
ATOM    565  CZ  TYR A 129      12.942  15.980  31.231  1.00 28.91
ATOM    566  OH  TYR A 129      13.634  14.896  30.751  1.00 30.21
ATOM    567  N   VAL A 130      13.620  20.782  31.602  1.00 19.35
ATOM    568  CA  VAL A 130      14.353  21.003  30.350  1.00 17.21
ATOM    569  C   VAL A 130      15.308  19.872  30.022  1.00 16.02
ATOM    570  O   VAL A 130      16.319  19.628  30.748  1.00 16.89
ATOM    571  CB  VAL A 130      15.136  22.334  30.370  1.00 17.86
ATOM    572  CG1 VAL A 130      15.934  22.485  29.075  1.00 15.31
ATOM    573  CG2 VAL A 130      14.163  23.505  30.525  1.00 15.67
ATOM    574  N   PRO A 131      15.013  19.136  28.945  1.00 14.83
ATOM    575  CA  PRO A 131      15.868  18.028  28.529  1.00 14.77
ATOM    576  C   PRO A 131      16.743  18.516  27.372  1.00 15.00
ATOM    577  O   PRO A 131      16.234  19.154  26.402  1.00 15.43
ATOM    578  CB  PRO A 131      14.857  16.971  28.106  1.00 13.57
ATOM    579  CG  PRO A 131      13.809  17.806  27.421  1.00 13.44
ATOM    580  CD  PRO A 131      13.706  19.078  28.262  1.00 13.99
ATOM    581  N   TYR A 132      18.043  18.268  27.465  1.00 14.75
ATOM    582  CA  TYR A 132      18.989  18.679  26.404  1.00 17.37
ATOM    583  C   TYR A 132      19.438  17.415  25.676  1.00 17.52
ATOM    584  O   TYR A 132      19.100  16.274  26.105  1.00 17.41
ATOM    585  CB  TYR A 132      20.211  19.369  27.020  1.00 16.93
ATOM    586  CG  TYR A 132      19.909  20.665  27.742  1.00 18.63
ATOM    587  CD1 TYR A 132      19.834  21.881  27.051  1.00 17.88
ATOM    588  CD2 TYR A 132      19.706  20.681  29.122  1.00 19.01
ATOM    589  CE1 TYR A 132      19.564  23.080  27.722  1.00 16.57
ATOM    590  CE2 TYR A 132      19.435  21.867  29.799  1.00 17.74
ATOM    591  CZ  TYR A 132      19.365  23.062  29.098  1.00 19.02
ATOM    592  OH  TYR A 132      19.083  24.229  29.782  1.00 18.23
ATOM    593  N   THR A 133      20.188  17.574  24.592  1.00 18.46
ATOM    594  CA  THR A 133      20.686  16.403  23.842  1.00 18.54
ATOM    595  C   THR A 133      21.525  15.580  24.812  1.00 20.42
ATOM    596  O   THR A 133      21.667  14.325  24.672  1.00 19.49
ATOM    597  CB  THR A 133      21.546  16.846  22.653  1.00 18.40
ATOM    598  OG1 THR A 133      20.720  17.539  21.708  1.00 20.46
ATOM    599  CG2 THR A 133      22.194  15.645  21.976  1.00 18.37
ATOM    600  N   GLN A 134      22.064  16.265  25.810  1.00 22.23
ATOM    601  CA  GLN A 134      22.890  15.624  26.842  1.00 24.27
ATOM    602  C   GLN A 134      22.723  16.406  28.140  1.00 23.32
ATOM    603  O   GLN A 134      23.179  17.580  28.252  1.00 21.03
ATOM    604  CB  GLN A 134      24.352  15.633  26.405  1.00 28.22
ATOM    605  CG  GLN A 134      25.140  14.412  26.808  1.00 32.76
ATOM    606  CD  GLN A 134      25.020  13.296  25.781  1.00 36.63
ATOM    607  OE1 GLN A 134      26.052  12.680  25.356  1.00 37.34
ATOM    608  NE2 GLN A 134      23.791  13.018  25.352  1.00 38.92
ATOM    609  N   GLY A 135      22.080  15.789  29.124  1.00 23.28
ATOM    610  CA  GLY A 135      21.863  16.460  30.391  1.00 21.50
ATOM    611  C   GLY A 135      20.432  16.946  30.483  1.00 22.11
ATOM    612  O   GLY A 135      19.735  17.111  29.435  1.00 20.68
ATOM    613  N   LYS A 136      19.968  17.190  31.703  1.00 22.97
ATOM    614  CA  LYS A 136      18.584  17.654  31.923  1.00 23.80
ATOM    615  C   LYS A 136      18.429  18.147  33.353  1.00 22.33
ATOM    616  O   LYS A 136      19.196  17.719  34.269  1.00 21.42
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ATOM	617	CB	LYS	A	136	17.606	16.501	31.677	1.00	25.37
ATOM	618	CG	LYS	A	136	17.823	15.310	32.607	1.00	28.29
ATOM	619	CD	LYS	A	136	16.804	14.196	32.374	1.00	31.54
ATOM	620	CE	LYS	A	136	16.955	13.570	31.000	1.00	34.21
ATOM	621	NZ	LYS	A	136	15.996	12.444	30.789	1.00	37.76
ATOM	622	N	TRP	A	137	17.470	19.040	33.573	1.00	21.02
ATOM	623	CA	TRP	A	137	17.214	19.562	34.928	1.00	20.75
ATOM	624	C	TRP	A	137	15.750	19.907	35.133	1.00	20.62
ATOM	625	O	TRP	A	137	14.951	19.978	34.153	1.00	20.05
ATOM	626	CB	TRP	A	137	18.077	20.800	35.231	1.00	18.46
ATOM	627	CG	TRP	A	137	17.960	21.937	34.248	1.00	18.02
ATOM	628	CD1	TRP	A	137	18.865	22.276	33.281	1.00	18.12
ATOM	629	CD2	TRP	A	137	16.881	22.879	34.134	1.00	17.27
ATOM	630	NE1	TRP	A	137	18.419	23.369	32.574	1.00	17.78
ATOM	631	CE2	TRP	A	137	17.204	23.758	33.074	1.00	17.40
ATOM	632	CE3	TRP	A	137	15.675	23.067	34.823	1.00	17.08
ATOM	633	CZ2	TRP	A	137	16.363	24.807	32.684	1.00	15.50
ATOM	634	CZ3	TRP	A	137	14.836	24.113	34.434	1.00	17.23
ATOM	635	CH2	TRP	A	137	15.188	24.968	33.373	1.00	17.46
ATOM	636	N	GLU	A	138	15.385	20.098	36.395	1.00	21.53
ATOM	637	CA	GLU	A	138	14.014	20.472	36.789	1.00	24.94
ATOM	638	C	GLU	A	138	14.166	21.642	37.745	1.00	23.18
ATOM	639	O	GLU	A	138	15.168	21.719	38.526	1.00	21.21
ATOM	640	CB	GLU	A	138	13.320	19.320	37.515	1.00	28.46
ATOM	641	CG	GLU	A	138	13.053	18.101	36.656	1.00	34.91
ATOM	642	CD	GLU	A	138	12.562	16.919	37.472	1.00	37.93
ATOM	643	OE1	GLU	A	138	12.175	15.897	36.864	1.00	40.28
ATOM	644	OE2	GLU	A	138	12.570	17.009	38.722	1.00	40.20
ATOM	645	N	GLY	A	139	13.214	22.559	37.711	1.00	22.13
ATOM	646	CA	GLY	A	139	13.298	23.693	38.604	1.00	22.60
ATOM	647	C	GLY	A	139	11.975	24.402	38.713	1.00	21.54
ATOM	648	O	GLY	A	139	10.949	23.953	38.116	1.00	23.29
ATOM	649	N	GLU	A	140	11.962	25.494	39.465	1.00	21.74
ATOM	650	CA	GLU	A	140	10.733	26.284	39.648	1.00	21.81
ATOM	651	C	GLU	A	140	10.900	27.646	38.998	1.00	19.04
ATOM	652	O	GLU	A	140	11.975	28.304	39.125	1.00	18.42
ATOM	653	CB	GLU	A	140	10.404	26.425	41.139	1.00	24.39
ATOM	654	CG	GLU	A	140	11.479	25.887	42.065	1.00	28.61
ATOM	655	CD	GLU	A	140	10.922	25.385	43.383	1.00	29.72
ATOM	656	OE1	GLU	A	140	10.311	24.297	43.389	1.00	31.43
ATOM	657	OE2	GLU	A	140	11.091	26.077	44.410	1.00	30.48
ATOM	658	N	LEU	A	141	9.870	28.071	38.278	1.00	16.35
ATOM	659	CA	LEU	A	141	9.901	29.360	37.585	1.00	15.48
ATOM	660	C	LEU	A	141	9.674	30.546	38.511	1.00	15.68
ATOM	661	O	LEU	A	141	8.832	30.499	39.466	1.00	13.45
ATOM	662	CB	LEU	A	141	8.864	29.376	36.460	1.00	15.23
ATOM	663	CG	LEU	A	141	9.145	28.412	35.300	1.00	16.27
ATOM	664	CD1	LEU	A	141	8.008	28.461	34.300	1.00	15.60
ATOM	665	CD2	LEU	A	141	10.458	28.785	34.627	1.00	16.48
ATOM	666	N	GLY	A	142	10.424	31.608	38.241	1.00	15.15
ATOM	667	CA	GLY	A	142	10.323	32.819	39.015	1.00	12.33
ATOM	668	C	GLY	A	142	10.845	33.953	38.167	1.00	14.67
ATOM	669	O	GLY	A	142	11.242	33.758	36.971	1.00	13.75
ATOM	670	N	THR	A	143	10.877	35.137	38.754	1.00	14.88
ATOM	671	CA	THR	A	143	11.354	36.324	38.050	1.00	15.26
ATOM	672	C	THR	A	143	12.262	37.103	39.008	1.00	14.53
ATOM	673	O	THR	A	143	12.119	36.991	40.269	1.00	13.46
ATOM	674	CB	THR	A	143	10.131	37.154	37.600	1.00	16.18
ATOM	675	OG1	THR	A	143	10.192	37.362	36.187	1.00	20.69
ATOM	676	CG2	THR	A	143	10.058	38.465	38.325	1.00	12.43
ATOM	677	N	ASP	A	144	13.202	37.866	38.466	1.00	14.22
ATOM	678	CA	ASP	A	144	14.117	38.652	39.321	1.00	15.38

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ATOM    679  C   ASP A 144      14.942  39.609  38.479  1.00 15.67
ATOM    680  O   ASP A 144      14.984  39.496  37.208  1.00 16.83
ATOM    681  CB  ASP A 144      15.063  37.721  40.086  1.00 15.20
ATOM    682  CG  ASP A 144      15.367  38.218  41.496  1.00 17.84
ATOM    683  OD1 ASP A 144      15.359  39.447  41.724  1.00 16.62
ATOM    684  OD2 ASP A 144      15.630  37.373  42.379  1.00 16.33
ATOM    685  N   LEU A 145      15.596  40.551  39.147  1.00 16.74
ATOM    686  CA  LEU A 145      16.442  41.537  38.454  1.00 18.66
ATOM    687  C   LEU A 145      17.757  40.854  38.101  1.00 20.21
ATOM    688  O   LEU A 145      18.381  40.147  38.961  1.00 21.75
ATOM    689  CB  LEU A 145      16.697  42.746  39.351  1.00 18.43
ATOM    690  CG  LEU A 145      15.452  43.522  39.786  1.00 19.69
ATOM    691  CD1 LEU A 145      15.878  44.720  40.628  1.00 19.11
ATOM    692  CD2 LEU A 145      14.660  43.971  38.557  1.00 18.50
ATOM    693  N   VAL A 146      18.186  41.030  36.858  1.00 20.48
ATOM    694  CA  VAL A 146      19.426  40.402  36.387  1.00 21.21
ATOM    695  C   VAL A 146      20.331  41.426  35.725  1.00 22.80
ATOM    696  O   VAL A 146      19.849  42.386  35.045  1.00 22.16
ATOM    697  CB  VAL A 146      19.118  39.265  35.373  1.00 20.39
ATOM    698  CG1 VAL A 146      20.405  38.575  34.941  1.00 20.39
ATOM    699  CG2 VAL A 146      18.163  38.261  35.998  1.00 17.90
ATOM    700  N   SER A 147      21.633  41.251  35.913  1.00 22.35
ATOM    701  CA  SER A 147      22.615  42.158  35.309  1.00 23.39
ATOM    702  C   SER A 147      23.829  41.383  34.833  1.00 21.77
ATOM    703  O   SER A 147      24.119  40.242  35.321  1.00 20.08
ATOM    704  CB  SER A 147      23.059  43.225  36.316  1.00 25.41
ATOM    705  OG  SER A 147      21.993  44.107  36.627  1.00 31.97
ATOM    706  N   ILE A 148      24.534  41.972  33.878  1.00 19.69
ATOM    707  CA  ILE A 148      25.757  41.377  33.329  1.00 19.14
ATOM    708  C   ILE A 148      26.853  42.405  33.614  1.00 18.85
ATOM    709  O   ILE A 148      27.021  43.408  32.853  1.00 17.87
ATOM    710  CB  ILE A 148      25.618  41.137  31.817  1.00 18.61
ATOM    711  CG1 ILE A 148      24.449  40.181  31.559  1.00 19.01
ATOM    712  CG2 ILE A 148      26.909  40.564  31.255  1.00 17.68
ATOM    713  CD1 ILE A 148      24.221  39.864  30.097  1.00 19.61
ATOM    714  N   PRO A 149      27.601  42.214  34.711  1.00 17.99
ATOM    715  CA  PRO A 149      28.679  43.134  35.095  1.00 21.17
ATOM    716  C   PRO A 149      29.523  43.638  33.926  1.00 22.18
ATOM    717  O   PRO A 149      29.800  44.869  33.823  1.00 24.08
ATOM    718  CB  PRO A 149      29.485  42.317  36.103  1.00 19.87
ATOM    719  CG  PRO A 149      28.404  41.529  36.797  1.00 19.57
ATOM    720  CD  PRO A 149      27.542  41.061  35.628  1.00 17.55
ATOM    721  N   HIS A 150      29.930  42.733  33.041  1.00 23.43
ATOM    722  CA  HIS A 150      30.748  43.119  31.869  1.00 23.84
ATOM    723  C   HIS A 150      29.933  43.067  30.588  1.00 24.47
ATOM    724  O   HIS A 150      30.334  42.431  29.566  1.00 25.89
ATOM    725  CB  HIS A 150      31.968  42.211  31.765  1.00 23.54
ATOM    726  CG  HIS A 150      32.880  42.313  32.945  1.00 26.15
ATOM    727  ND1 HIS A 150      33.619  43.446  33.216  1.00 27.28
ATOM    728  CD2 HIS A 150      33.149  41.439  33.943  1.00 26.32
ATOM    729  CE1 HIS A 150      34.305  43.264  34.330  1.00 27.48
ATOM    730  NE2 HIS A 150      34.038  42.055  34.791  1.00 28.01
ATOM    731  N   GLY A 151      28.785  43.727  30.630  1.00 25.49
ATOM    732  CA  GLY A 151      27.906  43.784  29.485  1.00 26.41
ATOM    733  C   GLY A 151      27.325  45.179  29.468  1.00 27.16
ATOM    734  O   GLY A 151      27.981  46.136  29.983  1.00 26.97
ATOM    735  N   PRO A 152      26.125  45.370  28.903  1.00 28.12
ATOM    736  CA  PRO A 152      25.540  46.712  28.880  1.00 28.75
ATOM    737  C   PRO A 152      25.219  47.165  30.304  1.00 30.53
ATOM    738  O   PRO A 152      24.844  46.331  31.182  1.00 28.62
ATOM    739  CB  PRO A 152      24.294  46.528  28.017  1.00 29.49
ATOM    740  CG  PRO A 152      23.897  45.105  28.303  1.00 29.85
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ATOM	741	CD	PRO	A	152	25.227	44.385	28.277	1.00	28.15
ATOM	742	N	ASN	A	153	25.375	48.457	30.560	1.00	33.03
ATOM	743	CA	ASN	A	153	25.111	49.016	31.902	1.00	34.39
ATOM	744	C	ASN	A	153	23.604	49.096	32.144	1.00	33.81
ATOM	745	O	ASN	A	153	23.009	50.218	32.222	1.00	33.63
ATOM	746	CB	ASN	A	153	25.755	50.401	32.009	1.00	37.16
ATOM	747	CG	ASN	A	153	25.680	50.978	33.406	1.00	38.88
ATOM	748	OD1	ASN	A	153	25.974	50.272	34.416	1.00	40.17
ATOM	749	ND2	ASN	A	153	25.309	52.251	33.504	1.00	39.91
ATOM	750	N	VAL	A	154	22.971	47.934	32.265	1.00	31.55
ATOM	751	CA	VAL	A	154	21.514	47.872	32.486	1.00	29.59
ATOM	752	C	VAL	A	154	21.113	46.739	33.418	1.00	29.47
ATOM	753	O	VAL	A	154	21.924	45.809	33.718	1.00	30.24
ATOM	754	CB	VAL	A	154	20.755	47.681	31.154	1.00	29.95
ATOM	755	CG1	VAL	A	154	20.990	48.875	30.242	1.00	29.70
ATOM	756	CG2	VAL	A	154	21.216	46.397	30.474	1.00	28.94
ATOM	757	N	THR	A	155	19.874	46.799	33.882	1.00	27.83
ATOM	758	CA	THR	A	155	19.323	45.773	34.779	1.00	27.61
ATOM	759	C	THR	A	155	17.918	45.472	34.296	1.00	26.01
ATOM	760	O	THR	A	155	17.114	46.413	34.041	1.00	27.70
ATOM	761	CB	THR	A	155	19.268	46.280	36.229	1.00	27.24
ATOM	762	OG1	THR	A	155	20.603	46.486	36.703	1.00	29.54
ATOM	763	CG2	THR	A	155	18.573	45.270	37.129	1.00	27.37
ATOM	764	N	VAL	A	156	17.592	44.197	34.143	1.00	24.69
ATOM	765	CA	VAL	A	156	16.241	43.847	33.672	1.00	24.32
ATOM	766	C	VAL	A	156	15.631	42.736	34.504	1.00	23.23
ATOM	767	O	VAL	A	156	16.364	41.920	35.154	1.00	23.57
ATOM	768	CB	VAL	A	156	16.253	43.402	32.184	1.00	25.34
ATOM	769	CG1	VAL	A	156	17.178	44.302	31.379	1.00	26.63
ATOM	770	CG2	VAL	A	156	16.684	41.960	32.063	1.00	24.89
ATOM	771	N	ARG	A	157	14.306	42.687	34.521	1.00	21.44
ATOM	772	CA	ARG	A	157	13.613	41.626	35.262	1.00	20.90
ATOM	773	C	ARG	A	157	13.374	40.560	34.215	1.00	20.13
ATOM	774	O	ARG	A	157	12.746	40.836	33.152	1.00	19.99
ATOM	775	CB	ARG	A	157	12.280	42.121	35.830	1.00	20.03
ATOM	776	CG	ARG	A	157	11.528	41.053	36.621	1.00	18.95
ATOM	777	CD	ARG	A	157	10.271	41.616	37.260	1.00	18.99
ATOM	778	NE	ARG	A	157	10.554	42.408	38.456	1.00	18.47
ATOM	779	CZ	ARG	A	157	10.973	41.902	39.613	1.00	19.19
ATOM	780	NH1	ARG	A	157	11.167	40.596	39.747	1.00	18.30
ATOM	781	NH2	ARG	A	157	11.178	42.703	40.650	1.00	15.82
ATOM	782	N	ALA	A	158	13.878	39.359	34.463	1.00	20.27
ATOM	783	CA	ALA	A	158	13.713	38.266	33.496	1.00	19.08
ATOM	784	C	ALA	A	158	13.279	36.986	34.175	1.00	19.45
ATOM	785	O	ALA	A	158	13.379	36.845	35.432	1.00	19.64
ATOM	786	CB	ALA	A	158	15.017	38.031	32.756	1.00	18.56
ATOM	787	N	ASN	A	159	12.792	36.053	33.370	1.00	18.08
ATOM	788	CA	ASN	A	159	12.363	34.756	33.876	1.00	18.21
ATOM	789	C	ASN	A	159	13.607	33.992	34.282	1.00	18.60
ATOM	790	O	ASN	A	159	14.666	34.033	33.577	1.00	19.42
ATOM	791	CB	ASN	A	159	11.601	33.992	32.797	1.00	16.91
ATOM	792	CG	ASN	A	159	10.282	34.647	32.459	1.00	18.46
ATOM	793	OD1	ASN	A	159	9.479	34.978	33.381	1.00	19.46
ATOM	794	ND2	ASN	A	159	10.020	34.848	31.174	1.00	16.51
ATOM	795	N	ILE	A	160	13.518	33.311	35.412	1.00	18.73
ATOM	796	CA	ILE	A	160	14.643	32.529	35.916	1.00	17.64
ATOM	797	C	ILE	A	160	14.112	31.191	36.373	1.00	19.09
ATOM	798	O	ILE	A	160	13.122	31.125	37.176	1.00	18.38
ATOM	799	CB	ILE	A	160	15.319	33.212	37.128	1.00	18.36
ATOM	800	CG1	ILE	A	160	15.764	34.629	36.758	1.00	17.90
ATOM	801	CG2	ILE	A	160	16.521	32.394	37.585	1.00	17.16
ATOM	802	CD1	ILE	A	160	16.521	35.336	37.875	1.00	18.56

ATOM	803	N	ALA	A	161	14.717	30.123	35.871	1.00	17.55
ATOM	804	CA	ALA	A	161	14.314	28.778	36.275	1.00	18.11
ATOM	805	C	ALA	A	161	15.267	28.394	37.399	1.00	18.26
ATOM	806	O	ALA	A	161	16.507	28.223	37.166	1.00	17.61
ATOM	807	CB	ALA	A	161	14.447	27.805	35.105	1.00	17.28
ATOM	808	N	ALA	A	162	14.737	28.283	38.614	1.00	17.99
ATOM	809	CA	ALA	A	162	15.567	27.901	39.775	1.00	18.02
ATOM	810	C	ALA	A	162	15.746	26.382	39.774	1.00	18.52
ATOM	811	O	ALA	A	162	14.835	25.619	40.207	1.00	18.43
ATOM	812	CB	ALA	A	162	14.897	28.359	41.067	1.00	17.36
ATOM	813	N	ILE	A	163	16.900	25.928	39.300	1.00	19.89
ATOM	814	CA	ILE	A	163	17.204	24.480	39.215	1.00	18.56
ATOM	815	C	ILE	A	163	17.314	23.802	40.577	1.00	20.34
ATOM	816	O	ILE	A	163	18.238	24.122	41.402	1.00	19.83
ATOM	817	CB	ILE	A	163	18.512	24.245	38.430	1.00	17.19
ATOM	818	CG1	ILE	A	163	18.347	24.753	36.994	1.00	16.02
ATOM	819	CG2	ILE	A	163	18.874	22.761	38.445	1.00	14.93
ATOM	820	CD1	ILE	A	163	19.628	24.735	36.174	1.00	16.24
ATOM	821	N	THR	A	164	16.409	22.860	40.826	1.00	20.42
ATOM	822	CA	THR	A	164	16.379	22.122	42.112	1.00	23.01
ATOM	823	C	THR	A	164	16.817	20.665	41.958	1.00	24.30
ATOM	824	O	THR	A	164	17.119	19.966	42.973	1.00	26.25
ATOM	825	CB	THR	A	164	14.966	22.173	42.735	1.00	22.01
ATOM	826	OG1	THR	A	164	13.990	21.799	41.754	1.00	22.15
ATOM	827	CG2	THR	A	164	14.656	23.584	43.214	1.00	22.73
ATOM	828	N	GLU	A	165	16.858	20.187	40.721	1.00	25.84
ATOM	829	CA	GLU	A	165	17.281	18.804	40.444	1.00	27.82
ATOM	830	C	GLU	A	165	17.800	18.693	39.024	1.00	26.80
ATOM	831	O	GLU	A	165	17.246	19.323	38.072	1.00	26.59
ATOM	832	CB	GLU	A	165	16.121	17.834	40.678	1.00	31.67
ATOM	833	CG	GLU	A	165	16.233	17.118	42.020	1.00	38.94
ATOM	834	CD	GLU	A	165	14.913	16.568	42.519	1.00	41.54
ATOM	835	OE1	GLU	A	165	14.282	15.765	41.796	1.00	44.35
ATOM	836	OE2	GLU	A	165	14.510	16.940	43.644	1.00	43.84
ATOM	837	N	SER	A	166	18.861	17.919	38.852	1.00	24.81
ATOM	838	CA	SER	A	166	19.455	17.765	37.525	1.00	25.32
ATOM	839	C	SER	A	166	20.213	16.459	37.397	1.00	25.44
ATOM	840	O	SER	A	166	20.551	15.795	38.427	1.00	24.00
ATOM	841	CB	SER	A	166	20.405	18.928	37.255	1.00	23.13
ATOM	842	OG	SER	A	166	21.444	18.939	38.217	1.00	21.22
ATOM	843	N	ASP	A	167	20.490	16.079	36.155	1.00	26.01
ATOM	844	CA	ASP	A	167	21.227	14.842	35.871	1.00	26.62
ATOM	845	C	ASP	A	167	22.138	15.038	34.671	1.00	25.62
ATOM	846	O	ASP	A	167	21.656	15.300	33.528	1.00	24.35
ATOM	847	CB	ASP	A	167	20.253	13.691	35.601	1.00	30.53
ATOM	848	CG	ASP	A	167	20.966	12.370	35.387	1.00	32.67
ATOM	849	OD1	ASP	A	167	21.912	12.083	36.152	1.00	36.14
ATOM	850	OD2	ASP	A	167	20.586	11.615	34.469	1.00	34.63
ATOM	851	N	LYS	A	168	23.440	14.930	34.910	1.00	25.32
ATOM	852	CA	LYS	A	168	24.461	15.078	33.847	1.00	25.94
ATOM	853	C	LYS	A	168	24.416	16.445	33.175	1.00	25.49
ATOM	854	O	LYS	A	168	24.742	16.580	31.955	1.00	25.50
ATOM	855	CB	LYS	A	168	24.282	13.979	32.800	1.00	27.68
ATOM	856	CG	LYS	A	168	24.408	12.570	33.362	1.00	30.33
ATOM	857	CD	LYS	A	168	24.117	11.532	32.292	1.00	32.36
ATOM	858	CE	LYS	A	168	24.205	10.126	32.855	1.00	34.37
ATOM	859	NZ	LYS	A	168	23.889	9.101	31.821	1.00	36.50
ATOM	860	N	PHE	A	169	24.024	17.460	33.937	1.00	22.87
ATOM	861	CA	PHE	A	169	23.942	18.835	33.418	1.00	20.96
ATOM	862	C	PHE	A	169	25.158	19.616	33.897	1.00	22.06
ATOM	863	O	PHE	A	169	25.983	20.119	33.069	1.00	20.71
ATOM	864	CB	PHE	A	169	22.668	19.506	33.919	1.00	19.76

ATOM	865	CG	PHE	A	169	22.526	20.931	33.479	1.00	18.95
ATOM	866	CD1	PHE	A	169	22.400	21.248	32.130	1.00	18.27
ATOM	867	CD2	PHE	A	169	22.525	21.963	34.416	1.00	18.36
ATOM	868	CE1	PHE	A	169	22.275	22.571	31.720	1.00	16.94
ATOM	869	CE2	PHE	A	169	22.401	23.287	34.013	1.00	17.25
ATOM	870	CZ	PHE	A	169	22.275	23.590	32.661	1.00	16.89
ATOM	871	N	PHE	A	170	25.292	19.738	35.212	1.00	20.46
ATOM	872	CA	PHE	A	170	26.438	20.452	35.788	1.00	21.45
ATOM	873	C	PHE	A	170	27.702	19.620	35.574	1.00	22.40
ATOM	874	O	PHE	A	170	27.675	18.355	35.665	1.00	22.55
ATOM	875	CB	PHE	A	170	26.205	20.705	37.281	1.00	19.44
ATOM	876	CG	PHE	A	170	25.079	21.663	37.559	1.00	18.44
ATOM	877	CD1	PHE	A	170	23.988	21.276	38.330	1.00	18.45
ATOM	878	CD2	PHE	A	170	25.098	22.948	37.025	1.00	16.73
ATOM	879	CE1	PHE	A	170	22.932	22.154	38.563	1.00	17.50
ATOM	880	CE2	PHE	A	170	24.046	23.832	37.253	1.00	17.78
ATOM	881	CZ	PHE	A	170	22.963	23.432	38.023	1.00	16.39
ATOM	882	N	ILE	A	171	28.805	20.297	35.272	1.00	23.10
ATOM	883	CA	ILE	A	171	30.095	19.615	35.043	1.00	22.87
ATOM	884	C	ILE	A	171	31.057	19.962	36.163	1.00	24.02
ATOM	885	O	ILE	A	171	31.222	21.162	36.537	1.00	22.48
ATOM	886	CB	ILE	A	171	30.729	20.048	33.704	1.00	24.70
ATOM	887	CG1	ILE	A	171	29.823	19.632	32.544	1.00	22.57
ATOM	888	CG2	ILE	A	171	32.123	19.434	33.558	1.00	22.35
ATOM	889	CD1	ILE	A	171	30.319	20.100	31.192	1.00	23.46
ATOM	890	N	ASN	A	172	31.702	18.942	36.709	1.00	27.12
ATOM	891	CA	ASN	A	172	32.657	19.143	37.809	1.00	30.01
ATOM	892	C	ASN	A	172	33.864	19.975	37.359	1.00	29.57
ATOM	893	O	ASN	A	172	34.616	19.574	36.418	1.00	29.20
ATOM	894	CB	ASN	A	172	33.105	17.779	38.337	1.00	31.92
ATOM	895	CG	ASN	A	172	33.913	17.885	39.608	1.00	34.74
ATOM	896	OD1	ASN	A	172	33.615	18.737	40.504	1.00	36.04
ATOM	897	ND2	ASN	A	172	34.927	17.034	39.734	1.00	36.14
ATOM	898	N	GLY	A	173	34.049	21.132	37.991	1.00	28.24
ATOM	899	CA	GLY	A	173	35.166	22.001	37.659	1.00	27.99
ATOM	900	C	GLY	A	173	34.973	22.938	36.476	1.00	28.87
ATOM	901	O	GLY	A	173	35.944	23.644	36.063	1.00	29.20
ATOM	902	N	SER	A	174	33.769	22.988	35.914	1.00	28.95
ATOM	903	CA	SER	A	174	33.498	23.880	34.748	1.00	29.13
ATOM	904	C	SER	A	174	33.524	25.348	35.168	1.00	27.92
ATOM	905	O	SER	A	174	33.878	26.255	34.354	1.00	29.51
ATOM	906	CB	SER	A	174	32.130	23.562	34.148	1.00	28.90
ATOM	907	OG	SER	A	174	31.102	23.922	35.054	1.00	30.49
ATOM	908	N	ASN	A	175	33.140	25.593	36.416	1.00	25.45
ATOM	909	CA	ASN	A	175	33.095	26.951	37.011	1.00	23.59
ATOM	910	C	ASN	A	175	31.855	27.767	36.647	1.00	21.71
ATOM	911	O	ASN	A	175	31.828	29.019	36.853	1.00	20.11
ATOM	912	CB	ASN	A	175	34.354	27.754	36.662	1.00	27.01
ATOM	913	CG	ASN	A	175	34.548	28.950	37.582	1.00	29.09
ATOM	914	OD1	ASN	A	175	34.648	28.794	38.840	1.00	30.19
ATOM	915	ND2	ASN	A	175	34.600	30.144	37.004	1.00	30.01
ATOM	916	N	TRP	A	176	30.841	27.121	36.078	1.00	16.70
ATOM	917	CA	TRP	A	176	29.590	27.847	35.790	1.00	18.41
ATOM	918	C	TRP	A	176	28.482	27.170	36.580	1.00	17.87
ATOM	919	O	TRP	A	176	28.534	25.927	36.838	1.00	15.45
ATOM	920	CB	TRP	A	176	29.248	27.888	34.292	1.00	16.48
ATOM	921	CG	TRP	A	176	29.257	26.588	33.563	1.00	17.63
ATOM	922	CD1	TRP	A	176	30.291	26.063	32.842	1.00	17.33
ATOM	923	CD2	TRP	A	176	28.165	25.668	33.425	1.00	17.78
ATOM	924	NE1	TRP	A	176	29.911	24.881	32.258	1.00	16.01
ATOM	925	CE2	TRP	A	176	28.612	24.613	32.599	1.00	16.95
ATOM	926	CE3	TRP	A	176	26.852	25.635	33.918	1.00	18.29

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ATOM    927  CZ2 TRP A 176      27.794  23.532  32.252  1.00 17.40
ATOM    928  CZ3 TRP A 176      26.034  24.557  33.573  1.00 19.02
ATOM    929  CH2 TRP A 176      26.512  23.521  32.747  1.00 19.06
ATOM    930  N   GLU A 177      27.496  27.950  37.005  1.00 18.68
ATOM    931  CA  GLU A 177      26.387  27.385  37.797  1.00 21.01
ATOM    932  C   GLU A 177      25.024  27.700  37.224  1.00 20.81
ATOM    933  O   GLU A 177      23.977  27.582  37.938  1.00 21.08
ATOM    934  CB  GLU A 177      26.461  27.869  39.250  1.00 22.84
ATOM    935  CG  GLU A 177      26.865  29.322  39.443  1.00 26.63
ATOM    936  CD  GLU A 177      28.377  29.531  39.446  1.00 27.90
ATOM    937  OE1 GLU A 177      29.121  28.568  39.726  1.00 28.44
ATOM    938  OE2 GLU A 177      28.818  30.670  39.186  1.00 28.24
ATOM    939  N   GLY A 178      25.007  28.088  35.953  1.00 18.48
ATOM    940  CA  GLY A 178      23.759  28.411  35.295  1.00 16.82
ATOM    941  C   GLY A 178      23.929  28.406  33.791  1.00 15.90
ATOM    942  O   GLY A 178      25.070  28.248  33.264  1.00 15.75
ATOM    943  N   ILE A 179      22.831  28.589  33.076  1.00 14.53
ATOM    944  CA  ILE A 179      22.882  28.588  31.610  1.00 14.26
ATOM    945  C   ILE A 179      22.007  29.701  31.057  1.00 14.53
ATOM    946  O   ILE A 179      20.896  29.980  31.603  1.00 15.23
ATOM    947  CB  ILE A 179      22.428  27.217  31.069  1.00 14.45
ATOM    948  CG1 ILE A 179      22.535  27.183  29.548  1.00 14.28
ATOM    949  CG2 ILE A 179      21.002  26.921  31.525  1.00 13.41
ATOM    950  CD1 ILE A 179      22.359  25.788  28.974  1.00 13.85
ATOM    951  N   LEU A 180      22.489  30.350  29.998  1.00 14.91
ATOM    952  CA  LEU A 180      21.763  31.464  29.353  1.00 14.24
ATOM    953  C   LEU A 180      21.311  31.050  27.961  1.00 15.19
ATOM    954  O   LEU A 180      22.117  31.115  26.973  1.00 15.79
ATOM    955  CB  LEU A 180      22.675  32.690  29.223  1.00 14.83
ATOM    956  CG  LEU A 180      22.078  34.107  29.257  1.00 16.59
ATOM    957  CD1 LEU A 180      22.902  34.996  28.351  1.00 15.04
ATOM    958  CD2 LEU A 180      20.622  34.120  28.818  1.00 17.08
ATOM    959  N   GLY A 181      20.057  30.621  27.851  1.00 15.40
ATOM    960  CA  GLY A 181      19.525  30.227  26.561  1.00 13.68
ATOM    961  C   GLY A 181      19.276  31.481  25.741  1.00 15.03
ATOM    962  O   GLY A 181      18.402  32.330  26.107  1.00 14.58
ATOM    963  N   LEU A 182      20.002  31.629  24.638  1.00 12.84
ATOM    964  CA  LEU A 182      19.859  32.831  23.787  1.00 13.53
ATOM    965  C   LEU A 182      19.029  32.646  22.521  1.00 14.25
ATOM    966  O   LEU A 182      18.883  33.607  21.701  1.00 13.52
ATOM    967  CB  LEU A 182      21.250  33.352  23.418  1.00 13.44
ATOM    968  CG  LEU A 182      22.036  33.949  24.583  1.00 11.84
ATOM    969  CD1 LEU A 182      23.506  34.067  24.211  1.00 11.17
ATOM    970  CD2 LEU A 182      21.450  35.311  24.936  1.00 12.14
ATOM    971  N   ALA A 183      18.491  31.449  22.322  1.00 15.12
ATOM    972  CA  ALA A 183      17.660  31.183  21.131  1.00 15.16
ATOM    973  C   ALA A 183      16.276  31.788  21.361  1.00 17.66
ATOM    974  O   ALA A 183      16.053  32.526  22.377  1.00 16.26
ATOM    975  CB  ALA A 183      17.557  29.684  20.875  1.00 14.23
ATOM    976  N   TYR A 184      15.338  31.487  20.466  1.00 18.41
ATOM    977  CA  TYR A 184      13.976  32.060  20.550  1.00 17.40
ATOM    978  C   TYR A 184      12.953  31.334  21.424  1.00 18.41
ATOM    979  O   TYR A 184      13.131  30.135  21.807  1.00 14.95
ATOM    980  CB  TYR A 184      13.411  32.237  19.138  1.00 18.07
ATOM    981  CG  TYR A 184      14.327  33.017  18.216  1.00 19.50
ATOM    982  CD1 TYR A 184      15.295  32.367  17.446  1.00 19.23
ATOM    983  CD2 TYR A 184      14.233  34.408  18.119  1.00 19.65
ATOM    984  CE1 TYR A 184      16.144  33.083  16.599  1.00 19.22
ATOM    985  CE2 TYR A 184      15.079  35.134  17.279  1.00 19.50
ATOM    986  CZ  TYR A 184      16.027  34.466  16.521  1.00 19.86
ATOM    987  OH  TYR A 184      16.842  35.185  15.670  1.00 20.69
ATOM    988  N   ALA A 185      11.873  32.046  21.734  1.00 16.29
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ATOM	989	CA	ALA	A	185	10.784	31.519	22.592	1.00 17.90
ATOM	990	C	ALA	A	185	10.185	30.221	22.068	1.00 17.38
ATOM	991	O	ALA	A	185	9.682	29.372	22.869	1.00 15.41
ATOM	992	CB	ALA	A	185	9.690	32.579	22.742	1.00 15.99
ATOM	993	N	GLU	A	186	10.232	30.046	20.751	1.00 20.56
ATOM	994	CA	GLU	A	186	9.679	28.846	20.086	1.00 23.43
ATOM	995	C	GLU	A	186	10.169	27.533	20.690	1.00 23.87
ATOM	996	O	GLU	A	186	9.448	26.486	20.619	1.00 24.67
ATOM	997	CB	GLU	A	186	10.009	28.887	18.591	1.00 27.60
ATOM	998	CG	GLU	A	186	9.447	27.729	17.786	1.00 32.42
ATOM	999	CD	GLU	A	186	7.941	27.593	17.923	1.00 36.08
ATOM	1000	OE1	GLU	A	186	7.255	28.633	18.041	1.00 39.03
ATOM	1001	OE2	GLU	A	186	7.439	26.448	17.900	1.00 37.05
ATOM	1002	N	ILE	A	187	11.363	27.540	21.283	1.00 22.31
ATOM	1003	CA	ILE	A	187	11.904	26.302	21.900	1.00 19.35
ATOM	1004	C	ILE	A	187	12.113	26.441	23.403	1.00 20.13
ATOM	1005	O	ILE	A	187	12.887	25.654	24.034	1.00 19.35
ATOM	1006	CB	ILE	A	187	13.241	25.872	21.248	1.00 19.03
ATOM	1007	CG1	ILE	A	187	14.270	26.998	21.355	1.00 18.36
ATOM	1008	CG2	ILE	A	187	13.008	25.488	19.795	1.00 19.03
ATOM	1009	CD1	ILE	A	187	15.627	26.635	20.780	1.00 17.45
ATOM	1010	N	ALA	A	188	11.441	27.416	23.999	1.00 19.82
ATOM	1011	CA	ALA	A	188	11.551	27.636	25.454	1.00 20.35
ATOM	1012	C	ALA	A	188	10.622	26.661	26.171	1.00 19.60
ATOM	1013	O	ALA	A	188	9.554	26.277	25.618	1.00 19.52
ATOM	1014	CB	ALA	A	188	11.160	29.083	25.793	1.00 17.16
ATOM	1015	N	ARG	A	189	11.004	26.231	27.372	1.00 20.77
ATOM	1016	CA	ARG	A	189	10.142	25.324	28.164	1.00 21.43
ATOM	1017	C	ARG	A	189	9.577	26.162	29.303	1.00 22.80
ATOM	1018	O	ARG	A	189	10.274	27.099	29.817	1.00 23.68
ATOM	1019	CB	ARG	A	189	10.949	24.151	28.753	1.00 22.36
ATOM	1020	CG	ARG	A	189	11.689	23.285	27.729	1.00 23.90
ATOM	1021	CD	ARG	A	189	10.765	22.818	26.624	1.00 24.33
ATOM	1022	NE	ARG	A	189	11.419	21.914	25.681	1.00 25.35
ATOM	1023	CZ	ARG	A	189	11.336	20.586	25.724	1.00 27.35
ATOM	1024	NH1	ARG	A	189	10.620	19.991	26.673	1.00 24.73
ATOM	1025	NH2	ARG	A	189	11.959	19.849	24.807	1.00 25.42
ATOM	1026	N	PRO	A	190	8.325	25.890	29.725	1.00 23.27
ATOM	1027	CA	PRO	A	190	7.442	24.830	29.216	1.00 23.21
ATOM	1028	C	PRO	A	190	6.826	25.110	27.849	1.00 23.72
ATOM	1029	O	PRO	A	190	6.458	24.157	27.101	1.00 23.77
ATOM	1030	CB	PRO	A	190	6.377	24.713	30.305	1.00 22.63
ATOM	1031	CG	PRO	A	190	6.285	26.115	30.830	1.00 24.33
ATOM	1032	CD	PRO	A	190	7.745	26.527	30.921	1.00 22.73
ATOM	1033	N	ASP	A	191	6.681	26.383	27.508	1.00 25.20
ATOM	1034	CA	ASP	A	191	6.107	26.754	26.202	1.00 25.89
ATOM	1035	C	ASP	A	191	6.653	28.106	25.770	1.00 25.76
ATOM	1036	O	ASP	A	191	7.488	28.716	26.498	1.00 24.40
ATOM	1037	CB	ASP	A	191	4.569	26.757	26.269	1.00 28.36
ATOM	1038	CG	ASP	A	191	4.024	27.697	27.323	1.00 30.16
ATOM	1039	OD1	ASP	A	191	2.887	27.468	27.783	1.00 33.88
ATOM	1040	OD2	ASP	A	191	4.714	28.669	27.686	1.00 30.53
ATOM	1041	N	ASP	A	192	6.214	28.596	24.617	1.00 26.01
ATOM	1042	CA	ASP	A	192	6.724	29.877	24.088	1.00 26.22
ATOM	1043	C	ASP	A	192	6.236	31.123	24.813	1.00 26.52
ATOM	1044	O	ASP	A	192	6.567	32.275	24.395	1.00 26.27
ATOM	1045	CB	ASP	A	192	6.419	29.985	22.589	1.00 27.69
ATOM	1046	CG	ASP	A	192	4.940	30.161	22.296	1.00 29.61
ATOM	1047	OD1	ASP	A	192	4.102	29.647	23.066	1.00 31.87
ATOM	1048	OD2	ASP	A	192	4.618	30.805	21.279	1.00 30.31
ATOM	1049	N	SER	A	193	5.470	30.947	25.885	1.00 24.46
ATOM	1050	CA	SER	A	193	4.988	32.117	26.645	1.00 24.21

ATOM	1051	C	SER	A	193	6.078	32.565	27.614	1.00	22.68
ATOM	1052	O	SER	A	193	6.082	33.740	28.082	1.00	22.41
ATOM	1053	CB	SER	A	193	3.701	31.787	27.415	1.00	25.67
ATOM	1054	OG	SER	A	193	3.910	30.774	28.386	1.00	27.13
ATOM	1055	N	LEU	A	194	7.009	31.670	27.932	1.00	20.84
ATOM	1056	CA	LEU	A	194	8.107	32.044	28.852	1.00	18.87
ATOM	1057	C	LEU	A	194	9.149	32.830	28.065	1.00	18.82
ATOM	1058	O	LEU	A	194	10.066	32.240	27.419	1.00	19.19
ATOM	1059	CB	LEU	A	194	8.758	30.809	29.469	1.00	17.48
ATOM	1060	CG	LEU	A	194	9.680	31.201	30.631	1.00	19.18
ATOM	1061	CD1	LEU	A	194	8.825	31.633	31.825	1.00	16.80
ATOM	1062	CD2	LEU	A	194	10.585	30.044	31.014	1.00	16.32
ATOM	1063	N	GLU	A	195	9.025	34.150	28.095	1.00	18.44
ATOM	1064	CA	GLU	A	195	9.949	35.029	27.369	1.00	18.80
ATOM	1065	C	GLU	A	195	11.415	34.777	27.733	1.00	19.02
ATOM	1066	O	GLU	A	195	11.791	34.754	28.953	1.00	17.72
ATOM	1067	CB	GLU	A	195	9.575	36.485	27.644	1.00	20.83
ATOM	1068	CG	GLU	A	195	10.514	37.512	27.047	1.00	23.03
ATOM	1069	CD	GLU	A	195	9.989	38.926	27.204	1.00	24.10
ATOM	1070	OE1	GLU	A	195	9.211	39.373	26.337	1.00	25.77
ATOM	1071	OE2	GLU	A	195	10.343	39.585	28.203	1.00	24.06
ATOM	1072	N	PRO	A	196	12.272	34.559	26.714	1.00	18.43
ATOM	1073	CA	PRO	A	196	13.702	34.311	26.935	1.00	18.17
ATOM	1074	C	PRO	A	196	14.385	35.571	27.447	1.00	16.90
ATOM	1075	O	PRO	A	196	13.845	36.715	27.297	1.00	17.67
ATOM	1076	CB	PRO	A	196	14.210	33.914	25.546	1.00	17.79
ATOM	1077	CG	PRO	A	196	12.992	33.305	24.892	1.00	19.11
ATOM	1078	CD	PRO	A	196	11.911	34.287	25.310	1.00	18.58
ATOM	1079	N	PHE	A	197	15.558	35.405	28.039	1.00	15.80
ATOM	1080	CA	PHE	A	197	16.290	36.550	28.574	1.00	14.47
ATOM	1081	C	PHE	A	197	16.597	37.663	27.576	1.00	16.31
ATOM	1082	O	PHE	A	197	16.392	38.873	27.894	1.00	14.87
ATOM	1083	CB	PHE	A	197	17.595	36.093	29.217	1.00	12.99
ATOM	1084	CG	PHE	A	197	18.472	37.227	29.652	1.00	13.09
ATOM	1085	CD1	PHE	A	197	19.376	37.806	28.767	1.00	12.33
ATOM	1086	CD2	PHE	A	197	18.347	37.766	30.926	1.00	14.29
ATOM	1087	CE1	PHE	A	197	20.139	38.907	29.143	1.00	12.22
ATOM	1088	CE2	PHE	A	197	19.108	38.873	31.310	1.00	14.64
ATOM	1089	CZ	PHE	A	197	20.002	39.441	30.415	1.00	13.26
ATOM	1090	N	PHE	A	198	17.089	37.319	26.390	1.00	16.71
ATOM	1091	CA	PHE	A	198	17.427	38.384	25.431	1.00	17.60
ATOM	1092	C	PHE	A	198	16.212	39.192	25.001	1.00	17.52
ATOM	1093	O	PHE	A	198	16.317	40.434	24.774	1.00	16.03
ATOM	1094	CB	PHE	A	198	18.133	37.829	24.196	1.00	17.77
ATOM	1095	CG	PHE	A	198	19.051	38.826	23.549	1.00	17.92
ATOM	1096	CD1	PHE	A	198	20.310	39.075	24.087	1.00	18.66
ATOM	1097	CD2	PHE	A	198	18.633	39.569	22.455	1.00	16.90
ATOM	1098	CE1	PHE	A	198	21.139	40.053	23.546	1.00	18.55
ATOM	1099	CE2	PHE	A	198	19.454	40.551	21.904	1.00	17.96
ATOM	1100	CZ	PHE	A	198	20.708	40.795	22.451	1.00	18.52
ATOM	1101	N	ASP	A	199	15.066	38.530	24.879	1.00	17.52
ATOM	1102	CA	ASP	A	199	13.819	39.225	24.491	1.00	19.54
ATOM	1103	C	ASP	A	199	13.464	40.261	25.561	1.00	18.83
ATOM	1104	O	ASP	A	199	13.134	41.444	25.233	1.00	20.48
ATOM	1105	CB	ASP	A	199	12.685	38.210	24.338	1.00	21.95
ATOM	1106	CG	ASP	A	199	12.868	37.312	23.126	1.00	24.77
ATOM	1107	OD1	ASP	A	199	12.408	37.687	22.028	1.00	27.27
ATOM	1108	OD2	ASP	A	199	13.481	36.234	23.261	1.00	27.11
ATOM	1109	N	SER	A	200	13.530	39.858	26.829	1.00	17.89
ATOM	1110	CA	SER	A	200	13.223	40.784	27.947	1.00	16.17
ATOM	1111	C	SER	A	200	14.211	41.943	27.915	1.00	16.77
ATOM	1112	O	SER	A	200	13.823	43.140	28.072	1.00	17.20

ATOM	1113	CB	SER	A	200	13.336	40.062	29.292	1.00 14.55
ATOM	1114	OG	SER	A	200	12.386	39.017	29.400	1.00 14.16
ATOM	1115	N	LEU	A	201	15.481	41.617	27.711	1.00 16.47
ATOM	1116	CA	LEU	A	201	16.553	42.638	27.654	1.00 18.93
ATOM	1117	C	LEU	A	201	16.237	43.684	26.586	1.00 18.88
ATOM	1118	O	LEU	A	201	16.274	44.917	26.852	1.00 18.26
ATOM	1119	CB	LEU	A	201	17.884	41.953	27.337	1.00 18.68
ATOM	1120	CG	LEU	A	201	19.244	42.637	27.523	1.00 20.59
ATOM	1121	CD1	LEU	A	201	19.973	42.616	26.194	1.00 20.98
ATOM	1122	CD2	LEU	A	201	19.100	44.053	28.045	1.00 20.13
ATOM	1123	N	VAL	A	202	15.919	43.222	25.383	1.00 20.38
ATOM	1124	CA	VAL	A	202	15.600	44.130	24.264	1.00 20.23
ATOM	1125	C	VAL	A	202	14.335	44.938	24.532	1.00 23.13
ATOM	1126	O	VAL	A	202	14.284	46.175	24.255	1.00 23.36
ATOM	1127	CB	VAL	A	202	15.433	43.337	22.948	1.00 19.84
ATOM	1128	CG1	VAL	A	202	14.830	44.228	21.855	1.00 17.60
ATOM	1129	CG2	VAL	A	202	16.792	42.804	22.502	1.00 16.36
ATOM	1130	N	LYS	A	203	13.315	44.285	25.074	1.00 24.15
ATOM	1131	CA	LYS	A	203	12.050	44.985	25.360	1.00 27.77
ATOM	1132	C	LYS	A	203	12.178	46.049	26.452	1.00 27.47
ATOM	1133	O	LYS	A	203	11.753	47.223	26.252	1.00 26.63
ATOM	1134	CB	LYS	A	203	10.970	43.973	25.746	1.00 29.55
ATOM	1135	CG	LYS	A	203	9.609	44.594	26.008	1.00 34.08
ATOM	1136	CD	LYS	A	203	8.497	43.798	25.335	1.00 36.82
ATOM	1137	CE	LYS	A	203	8.504	42.342	25.774	1.00 38.97
ATOM	1138	NZ	LYS	A	203	7.512	41.533	25.012	1.00 40.86
ATOM	1139	N	GLN	A	204	12.771	45.687	27.585	1.00 26.46
ATOM	1140	CA	GLN	A	204	12.910	46.632	28.721	1.00 26.94
ATOM	1141	C	GLN	A	204	14.125	47.542	28.614	1.00 28.51
ATOM	1142	O	GLN	A	204	14.479	48.264	29.600	1.00 30.36
ATOM	1143	CB	GLN	A	204	13.007	45.848	30.032	1.00 24.17
ATOM	1144	CG	GLN	A	204	11.980	44.739	30.170	1.00 20.78
ATOM	1145	CD	GLN	A	204	12.270	43.821	31.342	1.00 20.14
ATOM	1146	OE1	GLN	A	204	11.725	42.676	31.420	1.00 19.72
ATOM	1147	NE2	GLN	A	204	13.107	44.279	32.265	1.00 16.56
ATOM	1148	N	THR	A	205	14.762	47.568	27.453	1.00 28.58
ATOM	1149	CA	THR	A	205	15.979	48.375	27.306	1.00 29.06
ATOM	1150	C	THR	A	205	16.186	48.905	25.885	1.00 30.58
ATOM	1151	O	THR	A	205	15.427	48.525	24.940	1.00 30.23
ATOM	1152	CB	THR	A	205	17.175	47.501	27.772	1.00 29.85
ATOM	1153	OG1	THR	A	205	17.572	47.899	29.088	1.00 29.62
ATOM	1154	CG2	THR	A	205	18.328	47.576	26.823	1.00 29.03
ATOM	1155	N	HIS	A	206	17.175	49.784	25.711	1.00 31.92
ATOM	1156	CA	HIS	A	206	17.488	50.350	24.372	1.00 33.38
ATOM	1157	C	HIS	A	206	18.548	49.530	23.637	1.00 32.31
ATOM	1158	O	HIS	A	206	18.905	49.845	22.460	1.00 31.08
ATOM	1159	CB	HIS	A	206	17.975	51.799	24.487	1.00 36.39
ATOM	1160	CG	HIS	A	206	16.898	52.773	24.848	1.00 39.92
ATOM	1161	ND1	HIS	A	206	15.696	52.836	24.177	1.00 40.95
ATOM	1162	CD2	HIS	A	206	16.849	53.736	25.800	1.00 40.35
ATOM	1163	CE1	HIS	A	206	14.951	53.794	24.699	1.00 41.58
ATOM	1164	NE2	HIS	A	206	15.627	54.356	25.685	1.00 41.65
ATOM	1165	N	VAL	A	207	19.075	48.501	24.291	1.00 29.55
ATOM	1166	CA	VAL	A	207	20.097	47.639	23.651	1.00 28.49
ATOM	1167	C	VAL	A	207	19.511	47.083	22.354	1.00 26.27
ATOM	1168	O	VAL	A	207	18.415	46.441	22.358	1.00 26.26
ATOM	1169	CB	VAL	A	207	20.498	46.462	24.572	1.00 28.77
ATOM	1170	CG1	VAL	A	207	21.399	45.491	23.825	1.00 29.45
ATOM	1171	CG2	VAL	A	207	21.219	46.987	25.805	1.00 28.52
ATOM	1172	N	PRO	A	208	20.192	47.311	21.220	1.00 24.42
ATOM	1173	CA	PRO	A	208	19.683	46.804	19.944	1.00 23.82
ATOM	1174	C	PRO	A	208	19.547	45.284	19.914	1.00 22.81

ATOM	1175	O	PRO	A	208	20.290	44.545	20.630	1.00	21.12
ATOM	1176	CB	PRO	A	208	20.689	47.343	18.926	1.00	24.65
ATOM	1177	CG	PRO	A	208	21.927	47.510	19.711	1.00	25.77
ATOM	1178	CD	PRO	A	208	21.441	48.062	21.025	1.00	24.39
ATOM	1179	N	ASN	A	209	18.605	44.806	19.109	1.00	21.59
ATOM	1180	CA	ASN	A	209	18.322	43.362	18.995	1.00	20.43
ATOM	1181	C	ASN	A	209	19.390	42.599	18.222	1.00	20.52
ATOM	1182	O	ASN	A	209	19.190	42.217	17.026	1.00	21.39
ATOM	1183	CB	ASN	A	209	16.957	43.159	18.340	1.00	18.52
ATOM	1184	CG	ASN	A	209	16.501	41.728	18.402	1.00	18.12
ATOM	1185	OD1	ASN	A	209	16.968	40.948	19.281	1.00	18.32
ATOM	1186	ND2	ASN	A	209	15.594	41.348	17.513	1.00	15.63
ATOM	1187	N	LEU	A	210	20.514	42.346	18.883	1.00	19.53
ATOM	1188	CA	LEU	A	210	21.631	41.634	18.243	1.00	19.83
ATOM	1189	C	LEU	A	210	22.765	41.421	19.226	1.00	19.02
ATOM	1190	O	LEU	A	210	22.958	42.238	20.176	1.00	18.52
ATOM	1191	CB	LEU	A	210	22.120	42.451	17.035	1.00	21.93
ATOM	1192	CG	LEU	A	210	23.534	42.305	16.456	1.00	22.75
ATOM	1193	CD1	LEU	A	210	23.612	43.009	15.102	1.00	23.20
ATOM	1194	CD2	LEU	A	210	24.548	42.910	17.409	1.00	24.60
ATOM	1195	N	PHE	A	211	23.509	40.334	19.044	1.00	16.48
ATOM	1196	CA	PHE	A	211	24.671	40.055	19.909	1.00	16.70
ATOM	1197	C	PHE	A	211	25.722	39.310	19.095	1.00	16.08
ATOM	1198	O	PHE	A	211	25.392	38.653	18.063	1.00	17.22
ATOM	1199	CB	PHE	A	211	24.251	39.280	21.173	1.00	14.67
ATOM	1200	CG	PHE	A	211	23.813	37.863	20.924	1.00	16.01
ATOM	1201	CD1	PHE	A	211	24.748	36.837	20.835	1.00	14.91
ATOM	1202	CD2	PHE	A	211	22.465	37.546	20.824	1.00	14.62
ATOM	1203	CE1	PHE	A	211	24.344	35.515	20.653	1.00	15.05
ATOM	1204	CE2	PHE	A	211	22.054	36.224	20.641	1.00	15.47
ATOM	1205	CZ	PHE	A	211	22.996	35.207	20.558	1.00	12.73
ATOM	1206	N	SER	A	212	26.977	39.424	19.520	1.00	17.19
ATOM	1207	CA	SER	A	212	28.126	38.803	18.818	1.00	16.98
ATOM	1208	C	SER	A	212	28.894	37.862	19.725	1.00	16.10
ATOM	1209	O	SER	A	212	29.036	38.122	20.955	1.00	14.22
ATOM	1210	CB	SER	A	212	29.094	39.888	18.349	1.00	16.89
ATOM	1211	OG	SER	A	212	28.431	40.869	17.593	1.00	26.70
ATOM	1212	N	LEU	A	213	29.430	36.797	19.144	1.00	14.76
ATOM	1213	CA	LEU	A	213	30.194	35.819	19.930	1.00	14.81
ATOM	1214	C	LEU	A	213	31.563	35.509	19.352	1.00	14.32
ATOM	1215	O	LEU	A	213	31.702	35.162	18.137	1.00	12.74
ATOM	1216	CB	LEU	A	213	29.394	34.522	20.060	1.00	15.67
ATOM	1217	CG	LEU	A	213	28.735	34.210	21.408	1.00	18.95
ATOM	1218	CD1	LEU	A	213	28.196	35.475	22.050	1.00	18.65
ATOM	1219	CD2	LEU	A	213	27.627	33.185	21.192	1.00	16.46
ATOM	1220	N	GLN	A	214	32.581	35.656	20.191	1.00	14.19
ATOM	1221	CA	GLN	A	214	33.954	35.324	19.797	1.00	15.89
ATOM	1222	C	GLN	A	214	34.407	34.258	20.778	1.00	15.04
ATOM	1223	O	GLN	A	214	34.848	34.582	21.917	1.00	16.01
ATOM	1224	CB	GLN	A	214	34.903	36.523	19.914	1.00	17.92
ATOM	1225	CG	GLN	A	214	36.290	36.231	19.341	1.00	20.63
ATOM	1226	CD	GLN	A	214	37.397	37.099	19.932	1.00	23.22
ATOM	1227	OE1	GLN	A	214	38.459	37.332	19.273	1.00	24.79
ATOM	1228	NE2	GLN	A	214	37.199	37.571	21.156	1.00	24.53
ATOM	1229	N	LEU	A	215	34.284	32.997	20.390	1.00	14.37
ATOM	1230	CA	LEU	A	215	34.729	31.890	21.262	1.00	13.74
ATOM	1231	C	LEU	A	215	36.193	31.625	20.925	1.00	14.40
ATOM	1232	O	LEU	A	215	36.541	31.357	19.737	1.00	14.39
ATOM	1233	CB	LEU	A	215	33.872	30.644	21.005	1.00	13.94
ATOM	1234	CG	LEU	A	215	32.636	30.429	21.893	1.00	14.78
ATOM	1235	CD1	LEU	A	215	31.900	31.734	22.143	1.00	13.31
ATOM	1236	CD2	LEU	A	215	31.723	29.407	21.240	1.00	12.97

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ATOM   1237  N   CYS A 216      37.066  31.706  21.922  1.00 14.83
ATOM   1238  CA  CYS A 216      38.504  31.486  21.682  1.00 16.37
ATOM   1239  C   CYS A 216      39.066  30.196  22.263  1.00 17.20
ATOM   1240  O   CYS A 216      39.174  30.046  23.519  1.00 16.79
ATOM   1241  CB  CYS A 216      39.314  32.668  22.227  1.00 19.03
ATOM   1242  SG  CYS A 216      38.852  34.278  21.505  1.00 23.75
ATOM   1243  N   GLY A 217      39.415  29.257  21.387  1.00 15.43
ATOM   1244  CA  GLY A 217      40.018  28.021  21.843  1.00 16.40
ATOM   1245  C   GLY A 217      41.483  28.371  22.064  1.00 17.87
ATOM   1246  O   GLY A 217      42.057  29.204  21.303  1.00 17.53
ATOM   1247  N   ALA A 218      42.119  27.785  23.069  1.00 17.79
ATOM   1248  CA  ALA A 218      43.539  28.108  23.349  1.00 16.33
ATOM   1249  C   ALA A 218      44.486  27.408  22.379  1.00 17.71
ATOM   1250  O   ALA A 218      45.602  27.927  22.069  1.00 16.46
ATOM   1251  CB  ALA A 218      43.884  27.731  24.779  1.00 14.95
ATOM   1252  N   GLY A 219      44.073  26.245  21.890  1.00 16.19
ATOM   1253  CA  GLY A 219      44.909  25.505  20.970  1.00 17.57
ATOM   1254  C   GLY A 219      45.696  24.439  21.703  1.00 17.52
ATOM   1255  O   GLY A 219      46.490  23.675  21.076  1.00 16.29
ATOM   1256  N   PHE A 220      45.502  24.375  23.018  1.00 17.13
ATOM   1257  CA  PHE A 220      46.190  23.381  23.873  1.00 18.29
ATOM   1258  C   PHE A 220      45.381  23.185  25.153  1.00 19.24
ATOM   1259  O   PHE A 220      44.477  24.012  25.475  1.00 19.69
ATOM   1260  CB  PHE A 220      47.616  23.854  24.187  1.00 18.72
ATOM   1261  CG  PHE A 220      47.689  25.253  24.731  1.00 20.07
ATOM   1262  CD1 PHE A 220      47.448  25.507  26.077  1.00 20.91
ATOM   1263  CD2 PHE A 220      47.984  26.320  23.890  1.00 19.91
ATOM   1264  CE1 PHE A 220      47.505  26.809  26.576  1.00 21.79
ATOM   1265  CE2 PHE A 220      48.043  27.620  24.374  1.00 20.35
ATOM   1266  CZ  PHE A 220      47.802  27.866  25.721  1.00 21.77
ATOM   1267  N   PRO A 221      45.659  22.110  25.907  1.00 20.17
ATOM   1268  CA  PRO A 221      44.922  21.846  27.147  1.00 21.27
ATOM   1269  C   PRO A 221      45.014  22.959  28.180  1.00 23.04
ATOM   1270  O   PRO A 221      46.065  23.666  28.292  1.00 23.99
ATOM   1271  CB  PRO A 221      45.545  20.543  27.648  1.00 20.22
ATOM   1272  CG  PRO A 221      45.946  19.855  26.390  1.00 20.63
ATOM   1273  CD  PRO A 221      46.571  20.994  25.602  1.00 20.45
ATOM   1274  N   LEU A 222      43.934  23.132  28.933  1.00 25.72
ATOM   1275  CA  LEU A 222      43.873  24.158  29.991  1.00 28.32
ATOM   1276  C   LEU A 222      43.425  23.516  31.291  1.00 30.88
ATOM   1277  O   LEU A 222      42.248  23.042  31.403  1.00 31.71
ATOM   1278  CB  LEU A 222      42.880  25.261  29.620  1.00 27.52
ATOM   1279  CG  LEU A 222      43.264  26.233  28.506  1.00 27.30
ATOM   1280  CD1 LEU A 222      42.040  27.042  28.096  1.00 26.79
ATOM   1281  CD2 LEU A 222      44.382  27.143  28.983  1.00 27.13
ATOM   1282  N   ASN A 223      44.320  23.470  32.273  1.00 34.15
ATOM   1283  CA  ASN A 223      43.959  22.893  33.583  1.00 37.64
ATOM   1284  C   ASN A 223      43.014  23.882  34.254  1.00 38.54
ATOM   1285  O   ASN A 223      42.864  25.056  33.785  1.00 36.72
ATOM   1286  CB  ASN A 223      45.204  22.663  34.457  1.00 38.54
ATOM   1287  CG  ASN A 223      45.905  23.952  34.839  1.00 39.09
ATOM   1288  OD1 ASN A 223      45.268  24.903  35.375  1.00 41.39
ATOM   1289  ND2 ASN A 223      47.208  24.013  34.595  1.00 40.09
ATOM   1290  N   GLN A 224      42.380  23.444  35.335  1.00 41.79
ATOM   1291  CA  GLN A 224      41.415  24.278  36.073  1.00 43.58
ATOM   1292  C   GLN A 224      41.898  25.708  36.359  1.00 42.52
ATOM   1293  O   GLN A 224      41.138  26.705  36.126  1.00 42.75
ATOM   1294  CB  GLN A 224      41.021  23.572  37.378  1.00 46.22
ATOM   1295  CG  GLN A 224      39.629  23.956  37.827  1.00 49.86
ATOM   1296  CD  GLN A 224      39.085  23.160  38.990  1.00 51.40
ATOM   1297  OE1 GLN A 224      37.923  23.406  39.443  1.00 52.42
ATOM   1298  NE2 GLN A 224      39.866  22.215  39.496  1.00 52.75
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ATOM   1299  N   SER A 225      43.133  25.852  36.831  1.00 40.27
ATOM   1300  CA  SER A 225      43.669  27.200  37.138  1.00 39.30
ATOM   1301  C   SER A 225      43.989  28.028  35.893  1.00 36.57
ATOM   1302  O   SER A 225      43.920  29.292  35.930  1.00 36.27
ATOM   1303  CB  SER A 225      44.917  27.094  38.027  1.00 40.27
ATOM   1304  OG  SER A 225      45.974  26.411  37.376  1.00 42.21
ATOM   1305  N   GLU A 226      44.339  27.364  34.796  1.00 34.29
ATOM   1306  CA  GLU A 226      44.654  28.083  33.542  1.00 32.79
ATOM   1307  C   GLU A 226      43.375  28.651  32.954  1.00 31.17
ATOM   1308  O   GLU A 226      43.354  29.815  32.454  1.00 29.09
ATOM   1309  CB  GLU A 226      45.307  27.144  32.526  1.00 33.69
ATOM   1310  CG  GLU A 226      46.708  26.696  32.902  1.00 36.40
ATOM   1311  CD  GLU A 226      47.251  25.619  31.972  1.00 37.70
ATOM   1312  OE1 GLU A 226      46.585  24.567  31.830  1.00 37.54
ATOM   1313  OE2 GLU A 226      48.340  25.823  31.389  1.00 37.14
ATOM   1314  N   VAL A 227      42.305  27.867  33.007  1.00 29.89
ATOM   1315  CA  VAL A 227      41.013  28.312  32.458  1.00 30.15
ATOM   1316  C   VAL A 227      40.512  29.547  33.203  1.00 29.84
ATOM   1317  O   VAL A 227      39.922  30.484  32.582  1.00 30.30
ATOM   1318  CB  VAL A 227      39.940  27.210  32.558  1.00 30.93
ATOM   1319  CG1 VAL A 227      38.800  27.538  31.637  1.00 32.67
ATOM   1320  CG2 VAL A 227      40.516  25.867  32.183  1.00 32.31
ATOM   1321  N   LEU A 228      40.731  29.581  34.513  1.00 28.88
ATOM   1322  CA  LEU A 228      40.292  30.726  35.336  1.00 27.31
ATOM   1323  C   LEU A 228      41.059  31.992  34.975  1.00 27.59
ATOM   1324  O   LEU A 228      40.491  33.129  35.020  1.00 27.84
ATOM   1325  CB  LEU A 228      40.496  30.420  36.819  1.00 27.50
ATOM   1326  CG  LEU A 228      39.700  29.259  37.419  1.00 29.32
ATOM   1327  CD1 LEU A 228      40.129  29.053  38.867  1.00 28.16
ATOM   1328  CD2 LEU A 228      38.205  29.549  37.339  1.00 28.58
ATOM   1329  N   ALA A 229      42.327  31.835  34.610  1.00 27.12
ATOM   1330  CA  ALA A 229      43.176  32.998  34.257  1.00 27.64
ATOM   1331  C   ALA A 229      43.134  33.347  32.776  1.00 27.65
ATOM   1332  O   ALA A 229      43.460  34.504  32.375  1.00 29.94
ATOM   1333  CB  ALA A 229      44.617  32.736  34.682  1.00 27.52
ATOM   1334  N   SER A 230      42.736  32.393  31.947  1.00 26.68
ATOM   1335  CA  SER A 230      42.692  32.635  30.498  1.00 26.33
ATOM   1336  C   SER A 230      41.438  33.360  30.032  1.00 26.22
ATOM   1337  O   SER A 230      40.356  33.302  30.695  1.00 25.70
ATOM   1338  CB  SER A 230      42.815  31.310  29.746  1.00 26.07
ATOM   1339  OG  SER A 230      42.759  31.519  28.344  1.00 26.54
ATOM   1340  N   VAL A 231      41.562  34.056  28.909  1.00 25.03
ATOM   1341  CA  VAL A 231      40.415  34.764  28.320  1.00 24.89
ATOM   1342  C   VAL A 231      39.785  33.776  27.346  1.00 24.75
ATOM   1343  O   VAL A 231      40.453  33.310  26.371  1.00 25.97
ATOM   1344  CB  VAL A 231      40.859  36.043  27.568  1.00 24.38
ATOM   1345  CG1 VAL A 231      39.729  36.554  26.678  1.00 22.98
ATOM   1346  CG2 VAL A 231      41.244  37.119  28.577  1.00 23.20
ATOM   1347  N   GLY A 232      38.526  33.433  27.588  1.00 23.26
ATOM   1348  CA  GLY A 232      37.846  32.481  26.729  1.00 22.77
ATOM   1349  C   GLY A 232      37.125  33.081  25.538  1.00 21.57
ATOM   1350  O   GLY A 232      36.590  32.324  24.666  1.00 20.69
ATOM   1351  N   GLY A 233      37.078  34.408  25.468  1.00 19.21
ATOM   1352  CA  GLY A 233      36.410  35.050  24.353  1.00 17.96
ATOM   1353  C   GLY A 233      35.599  36.275  24.731  1.00 18.25
ATOM   1354  O   GLY A 233      35.778  36.866  25.851  1.00 15.19
ATOM   1355  N   SER A 234      34.708  36.677  23.828  1.00 16.58
ATOM   1356  CA  SER A 234      33.864  37.864  24.053  1.00 16.83
ATOM   1357  C   SER A 234      32.423  37.667  23.599  1.00 17.82
ATOM   1358  O   SER A 234      32.134  36.995  22.552  1.00 17.90
ATOM   1359  CB  SER A 234      34.426  39.072  23.291  1.00 16.36
ATOM   1360  OG  SER A 234      35.816  39.253  23.508  1.00 18.23
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ATOM	1361	N	MET	A	235	31.506	38.227	24.372	1.00 18.00
ATOM	1362	CA	MET	A	235	30.091	38.201	24.010	1.00 17.58
ATOM	1363	C	MET	A	235	29.732	39.677	23.996	1.00 18.27
ATOM	1364	O	MET	A	235	29.594	40.322	25.087	1.00 19.03
ATOM	1365	CB	MET	A	235	29.232	37.475	25.046	1.00 16.91
ATOM	1366	CG	MET	A	235	27.759	37.455	24.634	1.00 17.60
ATOM	1367	SD	MET	A	235	26.597	36.751	25.819	1.00 20.56
ATOM	1368	CE	MET	A	235	25.105	36.803	24.857	1.00 21.69
ATOM	1369	N	ILE	A	236	29.629	40.248	22.801	1.00 19.70
ATOM	1370	CA	ILE	A	236	29.271	41.669	22.674	1.00 19.40
ATOM	1371	C	ILE	A	236	27.764	41.758	22.522	1.00 20.06
ATOM	1372	O	ILE	A	236	27.175	41.365	21.467	1.00 16.87
ATOM	1373	CB	ILE	A	236	29.985	42.341	21.470	1.00 21.41
ATOM	1374	CG1	ILE	A	236	31.452	42.625	21.821	1.00 22.57
ATOM	1375	CG2	ILE	A	236	29.329	43.672	21.149	1.00 21.72
ATOM	1376	CD1	ILE	A	236	32.243	41.426	22.228	1.00 25.65
ATOM	1377	N	ILE	A	237	27.122	42.246	23.575	1.00 20.16
ATOM	1378	CA	ILE	A	237	25.663	42.382	23.599	1.00 21.01
ATOM	1379	C	ILE	A	237	25.215	43.710	22.996	1.00 22.16
ATOM	1380	O	ILE	A	237	25.620	44.812	23.472	1.00 22.96
ATOM	1381	CB	ILE	A	237	25.153	42.241	25.050	1.00 21.36
ATOM	1382	CG1	ILE	A	237	25.346	40.791	25.498	1.00 22.29
ATOM	1383	CG2	ILE	A	237	23.694	42.660	25.156	1.00 20.45
ATOM	1384	CD1	ILE	A	237	25.002	40.529	26.939	1.00 24.84
ATOM	1385	N	GLY	A	238	24.404	43.626	21.946	1.00 23.30
ATOM	1386	CA	GLY	A	238	23.903	44.820	21.288	1.00 25.11
ATOM	1387	C	GLY	A	238	24.821	45.437	20.244	1.00 26.35
ATOM	1388	O	GLY	A	238	24.644	46.640	19.874	1.00 27.08
ATOM	1389	N	GLY	A	239	25.792	44.681	19.743	1.00 25.50
ATOM	1390	CA	GLY	A	239	26.679	45.251	18.747	1.00 24.81
ATOM	1391	C	GLY	A	239	27.807	44.371	18.242	1.00 26.38
ATOM	1392	O	GLY	A	239	27.942	43.167	18.632	1.00 23.61
ATOM	1393	N	ILE	A	240	28.632	44.960	17.383	1.00 26.33
ATOM	1394	CA	ILE	A	240	29.780	44.273	16.758	1.00 25.87
ATOM	1395	C	ILE	A	240	31.067	45.033	17.055	1.00 26.95
ATOM	1396	O	ILE	A	240	31.121	46.287	16.882	1.00 28.86
ATOM	1397	CB	ILE	A	240	29.607	44.226	15.226	1.00 25.88
ATOM	1398	CG1	ILE	A	240	28.298	43.519	14.871	1.00 25.12
ATOM	1399	CG2	ILE	A	240	30.806	43.541	14.581	1.00 26.56
ATOM	1400	CD1	ILE	A	240	27.939	43.599	13.396	1.00 24.59
ATOM	1401	N	ASP	A	241	32.100	44.323	17.498	1.00 25.24
ATOM	1402	CA	ASP	A	241	33.395	44.973	17.781	1.00 25.13
ATOM	1403	C	ASP	A	241	34.383	44.548	16.698	1.00 26.31
ATOM	1404	O	ASP	A	241	34.676	43.326	16.536	1.00 26.89
ATOM	1405	CB	ASP	A	241	33.922	44.561	19.153	1.00 24.85
ATOM	1406	CG	ASP	A	241	35.171	45.325	19.541	1.00 24.81
ATOM	1407	OD1	ASP	A	241	35.144	46.032	20.567	1.00 27.86
ATOM	1408	OD2	ASP	A	241	36.180	45.226	18.817	1.00 25.69
ATOM	1409	N	HIS	A	242	34.913	45.517	15.960	1.00 26.86
ATOM	1410	CA	HIS	A	242	35.853	45.222	14.852	1.00 27.45
ATOM	1411	C	HIS	A	242	37.197	44.613	15.221	1.00 25.41
ATOM	1412	O	HIS	A	242	37.871	43.998	14.347	1.00 23.94
ATOM	1413	CB	HIS	A	242	36.085	46.481	14.013	1.00 32.38
ATOM	1414	CG	HIS	A	242	34.858	46.957	13.304	1.00 37.46
ATOM	1415	ND1	HIS	A	242	33.822	47.591	13.956	1.00 39.65
ATOM	1416	CD2	HIS	A	242	34.472	46.837	12.011	1.00 39.29
ATOM	1417	CE1	HIS	A	242	32.850	47.840	13.096	1.00 40.56
ATOM	1418	NE2	HIS	A	242	33.219	47.392	11.909	1.00 40.36
ATOM	1419	N	SER	A	243	37.615	44.751	16.471	1.00 22.23
ATOM	1420	CA	SER	A	243	38.915	44.184	16.877	1.00 22.06
ATOM	1421	C	SER	A	243	38.843	42.667	17.011	1.00 20.51
ATOM	1422	O	SER	A	243	39.897	41.986	17.130	1.00 23.23

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ATOM   1423  CB  SER A 243      39.368  44.785  18.211  1.00 22.47
ATOM   1424  OG  SER A 243      38.515  44.386  19.274  1.00 23.32
ATOM   1425  N   LEU A 244      37.635  42.115  16.979  1.00 20.52
ATOM   1426  CA  LEU A 244      37.454  40.649  17.145  1.00 18.32
ATOM   1427  C   LEU A 244      37.535  39.844  15.860  1.00 18.66
ATOM   1428  O   LEU A 244      37.482  38.576  15.892  1.00 18.25
ATOM   1429  CB  LEU A 244      36.120  40.368  17.843  1.00 18.01
ATOM   1430  CG  LEU A 244      35.998  41.054  19.206  1.00 17.93
ATOM   1431  CD1 LEU A 244      34.689  40.666  19.885  1.00 17.04
ATOM   1432  CD2 LEU A 244      37.189  40.661  20.063  1.00 19.23
ATOM   1433  N   TYR A 245      37.666  40.522  14.729  1.00 18.73
ATOM   1434  CA  TYR A 245      37.756  39.795  13.459  1.00 19.72
ATOM   1435  C   TYR A 245      38.536  40.545  12.398  1.00 20.55
ATOM   1436  O   TYR A 245      38.819  41.771  12.542  1.00 21.10
ATOM   1437  CB  TYR A 245      36.357  39.494  12.924  1.00 19.56
ATOM   1438  CG  TYR A 245      35.606  40.708  12.421  1.00 20.40
ATOM   1439  CD1 TYR A 245      34.977  41.586  13.302  1.00 20.11
ATOM   1440  CD2 TYR A 245      35.512  40.966  11.055  1.00 20.70
ATOM   1441  CE1 TYR A 245      34.265  42.689  12.834  1.00 21.90
ATOM   1442  CE2 TYR A 245      34.809  42.060  10.573  1.00 22.10
ATOM   1443  CZ  TYR A 245      34.184  42.919  11.466  1.00 23.05
ATOM   1444  OH  TYR A 245      33.476  43.993  10.979  1.00 22.53
ATOM   1445  N   THR A 246      38.902  39.829  11.340  1.00 20.48
ATOM   1446  CA  THR A 246      39.621  40.429  10.195  1.00 19.46
ATOM   1447  C   THR A 246      38.811  40.054   8.964  1.00 19.29
ATOM   1448  O   THR A 246      37.999  39.085   9.000  1.00 16.84
ATOM   1449  CB  THR A 246      41.049  39.865  10.031  1.00 19.69
ATOM   1450  OG1 THR A 246      40.997  38.434   9.953  1.00 20.05
ATOM   1451  CG2 THR A 246      41.929  40.294  11.194  1.00 19.01
ATOM   1452  N   GLY A 247      38.996  40.793   7.879  1.00 19.48
ATOM   1453  CA  GLY A 247      38.259  40.490   6.668  1.00 19.61
ATOM   1454  C   GLY A 247      36.812  40.927   6.747  1.00 20.26
ATOM   1455  O   GLY A 247      36.412  41.712   7.660  1.00 21.64
ATOM   1456  N   SER A 248      36.006  40.437   5.816  1.00 21.23
ATOM   1457  CA  SER A 248      34.580  40.806   5.765  1.00 23.54
ATOM   1458  C   SER A 248      33.649  39.836   6.484  1.00 23.00
ATOM   1459  O   SER A 248      33.978  38.625   6.684  1.00 21.96
ATOM   1460  CB  SER A 248      34.135  40.936   4.304  1.00 24.06
ATOM   1461  OG  SER A 248      34.814  41.999   3.656  1.00 28.27
ATOM   1462  N   LEU A 249      32.494  40.355   6.881  1.00 23.33
ATOM   1463  CA  LEU A 249      31.453  39.551   7.550  1.00 23.71
ATOM   1464  C   LEU A 249      30.478  39.103   6.468  1.00 23.26
ATOM   1465  O   LEU A 249      29.913  39.958   5.721  1.00 24.66
ATOM   1466  CB  LEU A 249      30.687  40.392   8.576  1.00 22.83
ATOM   1467  CG  LEU A 249      31.234  40.585   9.992  1.00 23.68
ATOM   1468  CD1 LEU A 249      30.483  41.728  10.659  1.00 23.07
ATOM   1469  CD2 LEU A 249      31.077  39.299  10.802  1.00 22.16
ATOM   1470  N   TRP A 250      30.285  37.797   6.335  1.00 21.28
ATOM   1471  CA  TRP A 250      29.328  37.282   5.348  1.00 18.03
ATOM   1472  C   TRP A 250      28.115  36.810   6.115  1.00 18.51
ATOM   1473  O   TRP A 250      28.242  36.079   7.153  1.00 18.65
ATOM   1474  CB  TRP A 250      29.925  36.128   4.550  1.00 19.15
ATOM   1475  CG  TRP A 250      30.759  36.597   3.411  1.00 19.10
ATOM   1476  CD1 TRP A 250      32.061  36.998   3.456  1.00 18.51
ATOM   1477  CD2 TRP A 250      30.328  36.777   2.058  1.00 18.74
ATOM   1478  NE1 TRP A 250      32.470  37.418   2.214  1.00 18.41
ATOM   1479  CE2 TRP A 250      31.425  37.294   1.336  1.00 18.71
ATOM   1480  CE3 TRP A 250      29.118  36.554   1.386  1.00 19.61
ATOM   1481  CZ2 TRP A 250      31.352  37.594  -0.029  1.00 18.57
ATOM   1482  CZ3 TRP A 250      29.043  36.853   0.026  1.00 20.92
ATOM   1483  CH2 TRP A 250      30.158  37.369  -0.666  1.00 17.98
ATOM   1484  N   TYR A 251      26.939  37.203   5.644  1.00 17.22
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ATOM	1485	CA	TYR	A	251	25.699	36.825	6.328	1.00 16.85
ATOM	1486	C	TYR	A	251	24.875	35.751	5.642	1.00 16.82
ATOM	1487	O	TYR	A	251	24.668	35.782	4.397	1.00 17.05
ATOM	1488	CB	TYR	A	251	24.814	38.059	6.536	1.00 17.46
ATOM	1489	CG	TYR	A	251	25.389	39.070	7.493	1.00 17.27
ATOM	1490	CD1	TYR	A	251	26.265	40.065	7.055	1.00 18.34
ATOM	1491	CD2	TYR	A	251	25.076	39.018	8.852	1.00 16.39
ATOM	1492	CE1	TYR	A	251	26.819	40.984	7.955	1.00 18.20
ATOM	1493	CE2	TYR	A	251	25.622	39.925	9.753	1.00 17.81
ATOM	1494	CZ	TYR	A	251	26.487	40.900	9.302	1.00 17.43
ATOM	1495	OH	TYR	A	251	27.014	41.779	10.215	1.00 20.25
ATOM	1496	N	THR	A	252	24.395	34.803	6.436	1.00 15.07
ATOM	1497	CA	THR	A	252	23.525	33.725	5.933	1.00 14.48
ATOM	1498	C	THR	A	252	22.204	33.996	6.646	1.00 16.15
ATOM	1499	O	THR	A	252	22.193	34.429	7.845	1.00 16.66
ATOM	1500	CB	THR	A	252	24.056	32.325	6.330	1.00 14.69
ATOM	1501	OG1	THR	A	252	23.273	31.316	5.684	1.00 13.97
ATOM	1502	CG2	THR	A	252	23.974	32.118	7.839	1.00 14.05
ATOM	1503	N	PRO	A	253	21.070	33.774	5.972	1.00 15.93
ATOM	1504	CA	PRO	A	253	19.826	34.054	6.694	1.00 17.09
ATOM	1505	C	PRO	A	253	19.418	33.029	7.741	1.00 18.67
ATOM	1506	O	PRO	A	253	19.782	31.813	7.653	1.00 17.11
ATOM	1507	CB	PRO	A	253	18.789	34.161	5.572	1.00 17.20
ATOM	1508	CG	PRO	A	253	19.304	33.207	4.545	1.00 17.18
ATOM	1509	CD	PRO	A	253	20.809	33.468	4.553	1.00 17.14
ATOM	1510	N	ILE	A	254	18.692	33.501	8.750	1.00 18.82
ATOM	1511	CA	ILE	A	254	18.165	32.604	9.792	1.00 20.14
ATOM	1512	C	ILE	A	254	16.885	32.091	9.137	1.00 21.33
ATOM	1513	O	ILE	A	254	15.911	32.875	8.914	1.00 21.52
ATOM	1514	CB	ILE	A	254	17.827	33.368	11.091	1.00 20.62
ATOM	1515	CG1	ILE	A	254	19.124	33.752	11.806	1.00 20.82
ATOM	1516	CG2	ILE	A	254	16.935	32.509	11.994	1.00 19.41
ATOM	1517	CD1	ILE	A	254	18.920	34.458	13.127	1.00 22.19
ATOM	1518	N	ARG	A	255	16.868	30.810	8.795	1.00 22.06
ATOM	1519	CA	ARG	A	255	15.702	30.211	8.115	1.00 23.47
ATOM	1520	C	ARG	A	255	14.398	30.343	8.880	1.00 24.68
ATOM	1521	O	ARG	A	255	13.334	30.719	8.299	1.00 25.49
ATOM	1522	CB	ARG	A	255	15.951	28.735	7.852	1.00 22.62
ATOM	1523	CG	ARG	A	255	14.843	28.093	7.053	1.00 22.10
ATOM	1524	CD	ARG	A	255	14.985	26.598	7.069	1.00 22.76
ATOM	1525	NE	ARG	A	255	14.031	25.958	6.176	1.00 22.51
ATOM	1526	CZ	ARG	A	255	13.692	24.679	6.256	1.00 22.37
ATOM	1527	NH1	ARG	A	255	14.232	23.914	7.195	1.00 20.91
ATOM	1528	NH2	ARG	A	255	12.819	24.166	5.396	1.00 23.78
ATOM	1529	N	ARG	A	256	14.451	30.023	10.165	1.00 24.98
ATOM	1530	CA	ARG	A	256	13.264	30.085	11.029	1.00 25.56
ATOM	1531	C	ARG	A	256	13.723	30.441	12.438	1.00 24.84
ATOM	1532	O	ARG	A	256	14.829	30.013	12.893	1.00 22.14
ATOM	1533	CB	ARG	A	256	12.561	28.729	11.009	1.00 27.37
ATOM	1534	CG	ARG	A	256	11.350	28.599	11.914	1.00 29.24
ATOM	1535	CD	ARG	A	256	10.878	27.150	11.899	1.00 29.60
ATOM	1536	NE	ARG	A	256	10.180	26.788	13.126	1.00 31.29
ATOM	1537	CZ	ARG	A	256	10.043	25.543	13.563	1.00 31.25
ATOM	1538	NH1	ARG	A	256	10.559	24.535	12.870	1.00 31.19
ATOM	1539	NH2	ARG	A	256	9.398	25.307	14.698	1.00 32.97
ATOM	1540	N	GLU	A	257	12.914	31.219	13.141	1.00 24.01
ATOM	1541	CA	GLU	A	257	13.270	31.650	14.500	1.00 23.46
ATOM	1542	C	GLU	A	257	12.829	30.739	15.636	1.00 23.02
ATOM	1543	O	GLU	A	257	11.749	30.947	16.264	1.00 26.15
ATOM	1544	CB	GLU	A	257	12.739	33.055	14.748	1.00 23.25
ATOM	1545	CG	GLU	A	257	13.439	34.123	13.930	1.00 26.24
ATOM	1546	CD	GLU	A	257	12.572	35.353	13.746	1.00 27.27

ATOM	1547	OE1	GLU	A	257	13.124	36.470	13.673	1.00 27.35
ATOM	1548	OE2	GLU	A	257	11.334	35.197	13.665	1.00 30.46
ATOM	1549	N	TRP	A	258	13.632	29.719	15.898	1.00 19.64
ATOM	1550	CA	TRP	A	258	13.390	28.798	17.016	1.00 19.75
ATOM	1551	C	TRP	A	258	14.812	28.548	17.495	1.00 19.46
ATOM	1552	O	TRP	A	258	15.267	29.190	18.500	1.00 20.47
ATOM	1553	CB	TRP	A	258	12.632	27.537	16.561	1.00 18.27
ATOM	1554	CG	TRP	A	258	13.203	26.710	15.455	1.00 17.96
ATOM	1555	CD1	TRP	A	258	13.898	27.143	14.364	1.00 18.43
ATOM	1556	CD2	TRP	A	258	13.051	25.293	15.298	1.00 17.87
ATOM	1557	NE1	TRP	A	258	14.187	26.082	13.537	1.00 18.62
ATOM	1558	CE2	TRP	A	258	13.678	24.935	14.088	1.00 17.86
ATOM	1559	CE3	TRP	A	258	12.441	24.291	16.067	1.00 17.50
ATOM	1560	CZ2	TRP	A	258	13.717	23.614	13.624	1.00 19.19
ATOM	1561	CZ3	TRP	A	258	12.477	22.976	15.608	1.00 19.16
ATOM	1562	CH2	TRP	A	258	13.113	22.650	14.396	1.00 18.86
ATOM	1563	N	TYR	A	259	15.538	27.670	16.814	1.00 18.33
ATOM	1564	CA	TYR	A	259	16.965	27.458	17.126	1.00 15.42
ATOM	1565	C	TYR	A	259	17.550	28.474	16.157	1.00 16.46
ATOM	1566	O	TYR	A	259	16.789	29.066	15.323	1.00 15.71
ATOM	1567	CB	TYR	A	259	17.439	26.078	16.671	1.00 13.86
ATOM	1568	CG	TYR	A	259	17.056	24.927	17.564	1.00 13.98
ATOM	1569	CD1	TYR	A	259	17.876	24.539	18.627	1.00 13.32
ATOM	1570	CD2	TYR	A	259	15.875	24.224	17.346	1.00 12.14
ATOM	1571	CE1	TYR	A	259	17.520	23.467	19.450	1.00 15.06
ATOM	1572	CE2	TYR	A	259	15.510	23.167	18.155	1.00 14.24
ATOM	1573	CZ	TYR	A	259	16.329	22.789	19.200	1.00 14.26
ATOM	1574	OH	TYR	A	259	15.940	21.719	19.955	1.00 12.92
ATOM	1575	N	TYR	A	260	18.851	28.725	16.224	1.00 14.50
ATOM	1576	CA	TYR	A	260	19.440	29.630	15.232	1.00 15.21
ATOM	1577	C	TYR	A	260	19.716	28.718	14.037	1.00 15.90
ATOM	1578	O	TYR	A	260	20.866	28.210	13.836	1.00 16.76
ATOM	1579	CB	TYR	A	260	20.722	30.269	15.759	1.00 13.84
ATOM	1580	CG	TYR	A	260	20.426	31.416	16.690	1.00 14.32
ATOM	1581	CD1	TYR	A	260	20.534	31.270	18.078	1.00 13.41
ATOM	1582	CD2	TYR	A	260	19.996	32.642	16.187	1.00 13.45
ATOM	1583	CE1	TYR	A	260	20.224	32.320	18.933	1.00 13.15
ATOM	1584	CE2	TYR	A	260	19.680	33.699	17.037	1.00 12.56
ATOM	1585	CZ	TYR	A	260	19.801	33.530	18.404	1.00 13.22
ATOM	1586	OH	TYR	A	260	19.531	34.582	19.239	1.00 12.88
ATOM	1587	N	GLU	A	261	18.664	28.476	13.260	1.00 15.81
ATOM	1588	CA	GLU	A	261	18.741	27.586	12.081	1.00 17.54
ATOM	1589	C	GLU	A	261	19.191	28.266	10.791	1.00 17.31
ATOM	1590	O	GLU	A	261	18.665	29.355	10.402	1.00 16.63
ATOM	1591	CB	GLU	A	261	17.382	26.914	11.842	1.00 16.53
ATOM	1592	CG	GLU	A	261	17.326	26.076	10.573	1.00 19.47
ATOM	1593	CD	GLU	A	261	15.965	25.454	10.326	1.00 20.18
ATOM	1594	OE1	GLU	A	261	14.956	26.037	10.766	1.00 21.27
ATOM	1595	OE2	GLU	A	261	15.902	24.390	9.673	1.00 20.94
ATOM	1596	N	VAL	A	262	20.153	27.640	10.122	1.00 16.45
ATOM	1597	CA	VAL	A	262	20.679	28.147	8.842	1.00 16.13
ATOM	1598	C	VAL	A	262	20.620	27.006	7.831	1.00 17.33
ATOM	1599	O	VAL	A	262	20.168	25.863	8.166	1.00 17.30
ATOM	1600	CB	VAL	A	262	22.131	28.624	8.982	1.00 14.58
ATOM	1601	CG1	VAL	A	262	22.218	29.690	10.064	1.00 14.84
ATOM	1602	CG2	VAL	A	262	23.039	27.449	9.308	1.00 14.53
ATOM	1603	N	ILE	A	263	21.064	27.271	6.608	1.00 17.34
ATOM	1604	CA	ILE	A	263	21.044	26.245	5.554	1.00 16.67
ATOM	1605	C	ILE	A	263	22.419	26.042	4.931	1.00 16.64
ATOM	1606	O	ILE	A	263	23.054	27.016	4.418	1.00 17.50
ATOM	1607	CB	ILE	A	263	20.031	26.619	4.445	1.00 18.45
ATOM	1608	CG1	ILE	A	263	18.608	26.522	4.996	1.00 18.90

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ATOM   1609  CG2 ILE A 263      20.192  25.694   3.243  1.00 18.17
ATOM   1610  CD1 ILE A 263      17.541  26.974   4.023  1.00 23.31
ATOM   1611  N   ILE A 264      22.897  24.802   4.988  1.00 16.67
ATOM   1612  CA  ILE A 264      24.199  24.413   4.409  1.00 14.63
ATOM   1613  C   ILE A 264      23.882  23.836   3.031  1.00 16.44
ATOM   1614  O   ILE A 264      23.019  22.915   2.908  1.00 13.53
ATOM   1615  CB  ILE A 264      24.877  23.320   5.253  1.00 14.79
ATOM   1616  CG1 ILE A 264      25.174  23.855   6.657  1.00 12.53
ATOM   1617  CG2 ILE A 264      26.154  22.846   4.563  1.00 12.07
ATOM   1618  CD1 ILE A 264      25.685  22.799   7.615  1.00 12.69
ATOM   1619  N   VAL A 265      24.546  24.334   1.992  1.00 17.37
ATOM   1620  CA  VAL A 265      24.258  23.841   0.627  1.00 18.64
ATOM   1621  C   VAL A 265      25.368  23.004   0.006  1.00 19.95
ATOM   1622  O   VAL A 265      25.202  22.455  -1.127  1.00 19.29
ATOM   1623  CB  VAL A 265      23.956  25.011  -0.322  1.00 18.56
ATOM   1624  CG1 VAL A 265      22.874  25.901   0.287  1.00 16.70
ATOM   1625  CG2 VAL A 265      25.227  25.802  -0.590  1.00 17.47
ATOM   1626  N   ARG A 266      26.486  22.872   0.707  1.00 20.42
ATOM   1627  CA  ARG A 266      27.617  22.098   0.165  1.00 20.48
ATOM   1628  C   ARG A 266      28.752  22.044   1.162  1.00 19.59
ATOM   1629  O   ARG A 266      29.030  23.055   1.885  1.00 19.51
ATOM   1630  CB  ARG A 266      28.112  22.763  -1.129  1.00 22.33
ATOM   1631  CG  ARG A 266      29.417  22.218  -1.713  1.00 22.40
ATOM   1632  CD  ARG A 266      29.939  23.170  -2.789  1.00 24.49
ATOM   1633  NE  ARG A 266      31.244  22.785  -3.322  1.00 24.49
ATOM   1634  CZ  ARG A 266      31.444  22.266  -4.528  1.00 26.46
ATOM   1635  NH1 ARG A 266      30.426  22.061  -5.349  1.00 25.31
ATOM   1636  NH2 ARG A 266      32.672  21.956  -4.920  1.00 27.88
ATOM   1637  N   VAL A 267      29.404  20.891   1.246  1.00 18.31
ATOM   1638  CA  VAL A 267      30.561  20.766   2.136  1.00 18.32
ATOM   1639  C   VAL A 267      31.671  20.072   1.369  1.00 18.25
ATOM   1640  O   VAL A 267      31.409  19.192   0.489  1.00 19.14
ATOM   1641  CB  VAL A 267      30.248  19.974   3.456  1.00 18.72
ATOM   1642  CG1 VAL A 267      28.784  19.645   3.547  1.00 18.30
ATOM   1643  CG2 VAL A 267      31.112  18.728   3.554  1.00 17.65
ATOM   1644  N   GLU A 268      32.903  20.471   1.647  1.00 16.18
ATOM   1645  CA  GLU A 268      34.046  19.848   0.990  1.00 17.71
ATOM   1646  C   GLU A 268      35.169  19.546   1.970  1.00 16.08
ATOM   1647  O   GLU A 268      35.293  20.191   3.064  1.00 13.62
ATOM   1648  CB  GLU A 268      34.550  20.717  -0.177  1.00 18.50
ATOM   1649  CG  GLU A 268      34.430  22.207   0.030  1.00 22.46
ATOM   1650  CD  GLU A 268      34.888  23.016  -1.181  1.00 22.13
ATOM   1651  OE1 GLU A 268      34.216  22.970  -2.237  1.00 20.91
ATOM   1652  OE2 GLU A 268      35.927  23.703  -1.067  1.00 22.44
ATOM   1653  N   ILE A 269      35.948  18.531   1.623  1.00 13.57
ATOM   1654  CA  ILE A 269      37.103  18.112   2.418  1.00 13.89
ATOM   1655  C   ILE A 269      38.259  18.448   1.485  1.00 14.06
ATOM   1656  O   ILE A 269      38.396  17.832   0.386  1.00 14.03
ATOM   1657  CB  ILE A 269      37.051  16.596   2.703  1.00 14.48
ATOM   1658  CG1 ILE A 269      35.697  16.239   3.327  1.00 14.59
ATOM   1659  CG2 ILE A 269      38.180  16.193   3.645  1.00 12.12
ATOM   1660  CD1 ILE A 269      35.358  17.022   4.592  1.00 13.16
ATOM   1661  N   ASN A 270      39.067  19.431   1.872  1.00 14.16
ATOM   1662  CA  ASN A 270      40.205  19.886   1.038  1.00 13.20
ATOM   1663  C   ASN A 270      39.774  20.177  -0.399  1.00 13.24
ATOM   1664  O   ASN A 270      40.427  19.714  -1.385  1.00 13.72
ATOM   1665  CB  ASN A 270      41.336  18.852   1.047  1.00 11.19
ATOM   1666  CG  ASN A 270      42.424  19.186   2.054  1.00 13.23
ATOM   1667  OD1 ASN A 270      42.339  20.224   2.790  1.00 13.62
ATOM   1668  ND2 ASN A 270      43.454  18.348   2.117  1.00 11.67
ATOM   1669  N   GLY A 271      38.691  20.932  -0.540  1.00 13.07
ATOM   1670  CA  GLY A 271      38.210  21.302  -1.858  1.00 13.58
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ATOM   1671  C   GLY A 271      37.393  20.241  -2.564  1.00 14.87
ATOM   1672  O   GLY A 271      36.704  20.545  -3.581  1.00 13.70
ATOM   1673  N   GLN A 272      37.447  19.005  -2.076  1.00 14.64
ATOM   1674  CA  GLN A 272      36.674  17.914  -2.705  1.00 14.45
ATOM   1675  C   GLN A 272      35.261  17.870  -2.140  1.00 15.83
ATOM   1676  O   GLN A 272      35.050  17.717  -0.902  1.00 15.81
ATOM   1677  CB  GLN A 272      37.357  16.561  -2.486  1.00 14.85
ATOM   1678  CG  GLN A 272      36.692  15.421  -3.250  1.00 14.45
ATOM   1679  CD  GLN A 272      37.499  14.135  -3.211  1.00 16.34
ATOM   1680  OE1 GLN A 272      37.097  13.134  -2.535  1.00 20.05
ATOM   1681  NE2 GLN A 272      38.633  14.121  -3.909  1.00 13.09
ATOM   1682  N   ASP A 273      34.291  17.995  -3.035  1.00 16.17
ATOM   1683  CA  ASP A 273      32.857  17.987  -2.686  1.00 17.89
ATOM   1684  C   ASP A 273      32.388  16.612  -2.201  1.00 16.92
ATOM   1685  O   ASP A 273      32.713  15.566  -2.831  1.00 16.53
ATOM   1686  CB  ASP A 273      32.060  18.395  -3.930  1.00 20.38
ATOM   1687  CG  ASP A 273      30.576  18.526  -3.665  1.00 20.89
ATOM   1688  OD1 ASP A 273      29.827  18.788  -4.630  1.00 21.98
ATOM   1689  OD2 ASP A 273      30.155  18.378  -2.503  1.00 22.40
ATOM   1690  N   LEU A 274      31.639  16.576  -1.101  1.00 17.95
ATOM   1691  CA  LEU A 274      31.117  15.285  -0.587  1.00 19.37
ATOM   1692  C   LEU A 274      30.092  14.805  -1.598  1.00 21.18
ATOM   1693  O   LEU A 274      29.702  13.603  -1.623  1.00 20.08
ATOM   1694  CB  LEU A 274      30.451  15.455   0.783  1.00 18.46
ATOM   1695  CG  LEU A 274      31.356  15.595   2.011  1.00 19.89
ATOM   1696  CD1 LEU A 274      30.489  15.558   3.267  1.00 17.23
ATOM   1697  CD2 LEU A 274      32.392  14.463   2.050  1.00 17.76
ATOM   1698  N   LYS A 275      29.646  15.736  -2.431  1.00 24.29
ATOM   1699  CA  LYS A 275      28.676  15.452  -3.501  1.00 29.08
ATOM   1700  C   LYS A 275      27.439  14.715  -3.000  1.00 28.92
ATOM   1701  O   LYS A 275      27.119  13.586  -3.464  1.00 30.50
ATOM   1702  CB  LYS A 275      29.360  14.642  -4.608  1.00 30.50
ATOM   1703  CG  LYS A 275      28.720  14.818  -5.970  1.00 33.82
ATOM   1704  CD  LYS A 275      29.476  14.059  -7.042  1.00 36.63
ATOM   1705  CE  LYS A 275      28.848  14.297  -8.408  1.00 38.29
ATOM   1706  NZ  LYS A 275      28.742  15.759  -8.702  1.00 39.43
ATOM   1707  N   MET A 276      26.734  15.329  -2.063  1.00 30.55
ATOM   1708  CA  MET A 276      25.519  14.722  -1.505  1.00 30.03
ATOM   1709  C   MET A 276      24.319  15.592  -1.815  1.00 30.11
ATOM   1710  O   MET A 276      24.465  16.818  -2.117  1.00 28.94
ATOM   1711  CB  MET A 276      25.641  14.576   0.011  1.00 30.29
ATOM   1712  CG  MET A 276      26.706  13.605   0.469  1.00 30.69
ATOM   1713  SD  MET A 276      26.687  13.418   2.261  1.00 32.94
ATOM   1714  CE  MET A 276      25.174  12.457   2.477  1.00 31.04
ATOM   1715  N   ASP A 277      23.136  14.994  -1.756  1.00 31.37
ATOM   1716  CA  ASP A 277      21.906  15.750  -1.994  1.00 33.34
ATOM   1717  C   ASP A 277      21.903  16.864  -0.955  1.00 33.96
ATOM   1718  O   ASP A 277      22.070  16.608   0.278  1.00 30.80
ATOM   1719  CB  ASP A 277      20.682  14.851  -1.818  1.00 36.24
ATOM   1720  CG  ASP A 277      19.377  15.595  -2.029  1.00 38.93
ATOM   1721  OD1 ASP A 277      18.332  14.925  -2.168  1.00 42.69
ATOM   1722  OD2 ASP A 277      19.386  16.844  -2.049  1.00 39.38
ATOM   1723  N   CYS A 278      21.732  18.089  -1.432  1.00 34.50
ATOM   1724  CA  CYS A 278      21.725  19.294  -0.581  1.00 37.44
ATOM   1725  C   CYS A 278      20.988  19.126   0.749  1.00 35.96
ATOM   1726  O   CYS A 278      21.503  19.540   1.834  1.00 34.38
ATOM   1727  CB  CYS A 278      21.108  20.460  -1.362  1.00 39.86
ATOM   1728  SG  CYS A 278      21.760  22.075  -0.852  1.00 50.09
ATOM   1729  N   LYS A 279      19.802  18.529   0.705  1.00 33.76
ATOM   1730  CA  LYS A 279      19.003  18.359   1.931  1.00 32.65
ATOM   1731  C   LYS A 279      19.584  17.430   2.996  1.00 30.06
ATOM   1732  O   LYS A 279      19.173  17.501   4.189  1.00 27.89
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ATOM	1733	CB	LYS	A	279	17.574	17.939	1.567	1.00	34.74
ATOM	1734	CG	LYS	A	279	17.459	16.765	0.612	1.00	39.08
ATOM	1735	CD	LYS	A	279	17.576	15.429	1.326	1.00	41.32
ATOM	1736	CE	LYS	A	279	17.185	14.289	0.393	1.00	42.86
ATOM	1737	NZ	LYS	A	279	17.118	12.978	1.099	1.00	45.07
ATOM	1738	N	GLU	A	280	20.525	16.570	2.621	1.00	27.06
ATOM	1739	CA	GLU	A	280	21.141	15.659	3.612	1.00	26.22
ATOM	1740	C	GLU	A	280	21.900	16.458	4.673	1.00	25.34
ATOM	1741	O	GLU	A	280	21.920	16.074	5.886	1.00	23.01
ATOM	1742	CB	GLU	A	280	22.109	14.693	2.928	1.00	27.98
ATOM	1743	CG	GLU	A	280	21.459	13.725	1.946	1.00	31.24
ATOM	1744	CD	GLU	A	280	20.486	12.765	2.610	1.00	32.55
ATOM	1745	OE1	GLU	A	280	20.447	12.704	3.857	1.00	33.21
ATOM	1746	OE2	GLU	A	280	19.763	12.058	1.878	1.00	34.72
ATOM	1747	N	TYR	A	281	22.515	17.562	4.255	1.00	23.32
ATOM	1748	CA	TYR	A	281	23.295	18.420	5.176	1.00	22.69
ATOM	1749	C	TYR	A	281	22.415	19.082	6.219	1.00	23.40
ATOM	1750	O	TYR	A	281	22.904	19.470	7.327	1.00	23.11
ATOM	1751	CB	TYR	A	281	24.035	19.515	4.400	1.00	20.26
ATOM	1752	CG	TYR	A	281	24.958	18.993	3.328	1.00	19.39
ATOM	1753	CD1	TYR	A	281	25.858	17.961	3.601	1.00	17.78
ATOM	1754	CD2	TYR	A	281	24.943	19.534	2.042	1.00	18.55
ATOM	1755	CE1	TYR	A	281	26.719	17.478	2.623	1.00	17.05
ATOM	1756	CE2	TYR	A	281	25.808	19.058	1.051	1.00	18.53
ATOM	1757	CZ	TYR	A	281	26.692	18.028	1.355	1.00	17.87
ATOM	1758	OH	TYR	A	281	27.558	17.533	0.407	1.00	18.13
ATOM	1759	N	ASN	A	282	21.136	19.232	5.899	1.00	22.82
ATOM	1760	CA	ASN	A	282	20.194	19.881	6.820	1.00	23.17
ATOM	1761	C	ASN	A	282	19.089	18.922	7.238	1.00	23.84
ATOM	1762	O	ASN	A	282	17.987	19.366	7.685	1.00	21.83
ATOM	1763	CB	ASN	A	282	19.598	21.111	6.137	1.00	22.42
ATOM	1764	CG	ASN	A	282	20.665	22.018	5.549	1.00	23.90
ATOM	1765	OD1	ASN	A	282	21.426	22.693	6.298	1.00	23.87
ATOM	1766	ND2	ASN	A	282	20.760	22.044	4.224	1.00	23.36
ATOM	1767	N	TYR	A	283	19.343	17.623	7.102	1.00	25.74
ATOM	1768	CA	TYR	A	283	18.322	16.633	7.472	1.00	28.01
ATOM	1769	C	TYR	A	283	17.905	16.843	8.912	1.00	29.29
ATOM	1770	O	TYR	A	283	18.686	16.572	9.881	1.00	27.50
ATOM	1771	CB	TYR	A	283	18.810	15.200	7.280	1.00	29.52
ATOM	1772	CG	TYR	A	283	17.783	14.200	7.756	1.00	31.64
ATOM	1773	CD1	TYR	A	283	16.428	14.374	7.460	1.00	32.38
ATOM	1774	CD2	TYR	A	283	18.153	13.098	8.523	1.00	33.44
ATOM	1775	CE1	TYR	A	283	15.468	13.479	7.919	1.00	33.96
ATOM	1776	CE2	TYR	A	283	17.201	12.194	8.987	1.00	35.48
ATOM	1777	CZ	TYR	A	283	15.860	12.392	8.683	1.00	35.35
ATOM	1778	OH	TYR	A	283	14.918	11.504	9.149	1.00	36.54
ATOM	1779	N	ASP	A	284	16.665	17.299	9.043	1.00	30.23
ATOM	1780	CA	ASP	A	284	16.026	17.638	10.312	1.00	28.41
ATOM	1781	C	ASP	A	284	16.273	19.129	10.409	1.00	27.12
ATOM	1782	O	ASP	A	284	15.309	19.953	10.305	1.00	25.19
ATOM	1783	CB	ASP	A	284	16.684	16.928	11.494	1.00	33.07
ATOM	1784	CG	ASP	A	284	16.035	17.283	12.813	1.00	33.49
ATOM	1785	OD1	ASP	A	284	16.520	16.815	13.860	1.00	37.38
ATOM	1786	OD2	ASP	A	284	15.035	18.031	12.802	1.00	35.95
ATOM	1787	N	LYS	A	285	17.542	19.499	10.563	1.00	22.62
ATOM	1788	CA	LYS	A	285	17.914	20.927	10.678	1.00	20.42
ATOM	1789	C	LYS	A	285	19.420	21.145	10.812	1.00	19.89
ATOM	1790	O	LYS	A	285	20.209	20.174	11.037	1.00	19.63
ATOM	1791	CB	LYS	A	285	17.230	21.540	11.903	1.00	18.63
ATOM	1792	CG	LYS	A	285	17.753	20.987	13.232	1.00	16.63
ATOM	1793	CD	LYS	A	285	16.966	21.538	14.421	1.00	14.93
ATOM	1794	CE	LYS	A	285	17.551	21.088	15.754	1.00	15.57

ATOM	1795	NZ	LYS	A	285	17.482	19.606	15.974	1.00	13.50
ATOM	1796	N	SER	A	286	19.827	22.402	10.678	1.00	17.19
ATOM	1797	CA	SER	A	286	21.241	22.808	10.827	1.00	16.52
ATOM	1798	C	SER	A	286	21.228	24.034	11.727	1.00	15.74
ATOM	1799	O	SER	A	286	20.592	25.080	11.377	1.00	14.46
ATOM	1800	CB	SER	A	286	21.862	23.179	9.475	1.00	16.90
ATOM	1801	OG	SER	A	286	22.064	22.036	8.671	1.00	16.60
ATOM	1802	N	ILE	A	287	21.900	23.946	12.870	1.00	13.25
ATOM	1803	CA	ILE	A	287	21.933	25.079	13.805	1.00	13.97
ATOM	1804	C	ILE	A	287	23.342	25.511	14.206	1.00	15.14
ATOM	1805	O	ILE	A	287	24.346	24.750	14.024	1.00	14.63
ATOM	1806	CB	ILE	A	287	21.145	24.757	15.102	1.00	13.55
ATOM	1807	CG1	ILE	A	287	21.898	23.717	15.929	1.00	12.52
ATOM	1808	CG2	ILE	A	287	19.758	24.214	14.754	1.00	12.10
ATOM	1809	CD1	ILE	A	287	21.274	23.455	17.283	1.00	14.43
ATOM	1810	N	VAL	A	288	23.431	26.728	14.732	1.00	14.78
ATOM	1811	CA	VAL	A	288	24.701	27.292	15.223	1.00	15.54
ATOM	1812	C	VAL	A	288	24.510	27.262	16.733	1.00	16.05
ATOM	1813	O	VAL	A	288	23.571	27.930	17.278	1.00	15.61
ATOM	1814	CB	VAL	A	288	24.896	28.751	14.767	1.00	15.19
ATOM	1815	CG1	VAL	A	288	26.248	29.259	15.239	1.00	14.78
ATOM	1816	CG2	VAL	A	288	24.791	28.842	13.246	1.00	15.19
ATOM	1817	N	ASP	A	289	25.355	26.512	17.430	1.00	15.91
ATOM	1818	CA	ASP	A	289	25.194	26.373	18.891	1.00	14.81
ATOM	1819	C	ASP	A	289	26.467	26.444	19.724	1.00	15.27
ATOM	1820	O	ASP	A	289	27.322	25.504	19.700	1.00	15.75
ATOM	1821	CB	ASP	A	289	24.467	25.060	19.168	1.00	12.65
ATOM	1822	CG	ASP	A	289	24.264	24.806	20.634	1.00	13.29
ATOM	1823	OD1	ASP	A	289	24.372	25.768	21.426	1.00	11.88
ATOM	1824	OD2	ASP	A	289	23.981	23.639	20.988	1.00	10.63
ATOM	1825	N	SER	A	290	26.604	27.529	20.479	1.00	15.19
ATOM	1826	CA	SER	A	290	27.782	27.730	21.346	1.00	14.55
ATOM	1827	C	SER	A	290	27.770	26.748	22.510	1.00	15.43
ATOM	1828	O	SER	A	290	28.823	26.539	23.186	1.00	13.77
ATOM	1829	CB	SER	A	290	27.795	29.165	21.888	1.00	15.33
ATOM	1830	OG	SER	A	290	26.614	29.442	22.620	1.00	12.79
ATOM	1831	N	GLY	A	291	26.612	26.137	22.759	1.00	14.34
ATOM	1832	CA	GLY	A	291	26.486	25.192	23.856	1.00	14.93
ATOM	1833	C	GLY	A	291	26.779	23.751	23.479	1.00	16.64
ATOM	1834	O	GLY	A	291	26.502	22.792	24.277	1.00	14.49
ATOM	1835	N	THR	A	292	27.305	23.556	22.277	1.00	16.47
ATOM	1836	CA	THR	A	292	27.674	22.202	21.812	1.00	15.30
ATOM	1837	C	THR	A	292	29.159	22.215	21.482	1.00	14.67
ATOM	1838	O	THR	A	292	29.653	23.102	20.725	1.00	13.26
ATOM	1839	CB	THR	A	292	26.889	21.784	20.550	1.00	15.29
ATOM	1840	OG1	THR	A	292	25.522	21.521	20.895	1.00	13.88
ATOM	1841	CG2	THR	A	292	27.514	20.527	19.932	1.00	13.59
ATOM	1842	N	THR	A	293	29.887	21.253	22.027	1.00	14.43
ATOM	1843	CA	THR	A	293	31.343	21.162	21.801	1.00	12.76
ATOM	1844	C	THR	A	293	31.749	20.906	20.348	1.00	14.47
ATOM	1845	O	THR	A	293	32.478	21.735	19.712	1.00	14.61
ATOM	1846	CB	THR	A	293	31.949	20.035	22.650	1.00	12.36
ATOM	1847	OG1	THR	A	293	31.726	20.304	24.041	1.00	10.79
ATOM	1848	CG2	THR	A	293	33.437	19.916	22.382	1.00	9.56
ATOM	1849	N	ASN	A	294	31.286	19.783	19.810	1.00	13.53
ATOM	1850	CA	ASN	A	294	31.648	19.349	18.440	1.00	15.26
ATOM	1851	C	ASN	A	294	30.871	19.917	17.276	1.00	15.45
ATOM	1852	O	ASN	A	294	29.851	20.662	17.431	1.00	13.68
ATOM	1853	CB	ASN	A	294	31.494	17.832	18.307	1.00	14.81
ATOM	1854	CG	ASN	A	294	32.351	17.051	19.270	1.00	14.13
ATOM	1855	OD1	ASN	A	294	32.264	15.791	19.304	1.00	19.85
ATOM	1856	ND2	ASN	A	294	33.174	17.734	20.051	1.00	13.25

ATOM	1857	N	LEU	A	295	31.365	19.556	16.096	1.00 15.21
ATOM	1858	CA	LEU	A	295	30.689	19.866	14.835	1.00 15.29
ATOM	1859	C	LEU	A	295	29.924	18.548	14.719	1.00 16.43
ATOM	1860	O	LEU	A	295	30.556	17.452	14.575	1.00 16.34
ATOM	1861	CB	LEU	A	295	31.674	19.963	13.671	1.00 13.54
ATOM	1862	CG	LEU	A	295	31.017	19.837	12.287	1.00 14.74
ATOM	1863	CD1	LEU	A	295	29.991	20.947	12.109	1.00 14.37
ATOM	1864	CD2	LEU	A	295	32.073	19.903	11.179	1.00 13.91
ATOM	1865	N	ARG	A	296	28.606	18.591	14.831	1.00 16.08
ATOM	1866	CA	ARG	A	296	27.827	17.349	14.719	1.00 17.47
ATOM	1867	C	ARG	A	296	27.180	17.300	13.343	1.00 17.04
ATOM	1868	O	ARG	A	296	26.655	18.339	12.840	1.00 15.28
ATOM	1869	CB	ARG	A	296	26.785	17.290	15.834	1.00 18.37
ATOM	1870	CG	ARG	A	296	27.421	17.444	17.208	1.00 19.73
ATOM	1871	CD	ARG	A	296	26.425	17.262	18.324	1.00 22.63
ATOM	1872	NE	ARG	A	296	26.292	15.867	18.722	1.00 25.23
ATOM	1873	CZ	ARG	A	296	25.135	15.223	18.776	1.00 26.52
ATOM	1874	NH1	ARG	A	296	24.011	15.851	18.446	1.00 27.11
ATOM	1875	NH2	ARG	A	296	25.100	13.961	19.179	1.00 27.00
ATOM	1876	N	LEU	A	297	27.211	16.123	12.722	1.00 15.65
ATOM	1877	CA	LEU	A	297	26.660	15.945	11.356	1.00 15.33
ATOM	1878	C	LEU	A	297	25.657	14.800	11.246	1.00 17.46
ATOM	1879	O	LEU	A	297	25.795	13.743	11.938	1.00 16.37
ATOM	1880	CB	LEU	A	297	27.806	15.681	10.371	1.00 12.00
ATOM	1881	CG	LEU	A	297	28.925	16.729	10.277	1.00 11.84
ATOM	1882	CD1	LEU	A	297	30.136	16.148	9.561	1.00 8.16
ATOM	1883	CD2	LEU	A	297	28.410	17.962	9.559	1.00 8.99
ATOM	1884	N	PRO	A	298	24.636	14.960	10.386	1.00 19.11
ATOM	1885	CA	PRO	A	298	23.636	13.901	10.217	1.00 20.53
ATOM	1886	C	PRO	A	298	24.387	12.619	9.868	1.00 21.03
ATOM	1887	O	PRO	A	298	25.419	12.668	9.131	1.00 21.77
ATOM	1888	CB	PRO	A	298	22.788	14.411	9.054	1.00 19.18
ATOM	1889	CG	PRO	A	298	22.861	15.897	9.209	1.00 20.46
ATOM	1890	CD	PRO	A	298	24.335	16.111	9.517	1.00 19.69
ATOM	1891	N	LYS	A	299	23.911	11.487	10.376	1.00 22.77
ATOM	1892	CA	LYS	A	299	24.562	10.169	10.137	1.00 25.34
ATOM	1893	C	LYS	A	299	25.169	9.979	8.753	1.00 24.56
ATOM	1894	O	LYS	A	299	26.393	9.681	8.617	1.00 22.24
ATOM	1895	CB	LYS	A	299	23.566	9.034	10.387	1.00 29.05
ATOM	1896	CG	LYS	A	299	24.156	7.650	10.146	1.00 33.27
ATOM	1897	CD	LYS	A	299	23.144	6.547	10.408	1.00 37.10
ATOM	1898	CE	LYS	A	299	23.758	5.178	10.151	1.00 38.78
ATOM	1899	NZ	LYS	A	299	22.775	4.077	10.380	1.00 42.51
ATOM	1900	N	LYS	A	300	24.340	10.127	7.729	1.00 24.24
ATOM	1901	CA	LYS	A	300	24.774	9.955	6.333	1.00 25.41
ATOM	1902	C	LYS	A	300	25.901	10.916	5.952	1.00 24.12
ATOM	1903	O	LYS	A	300	26.889	10.515	5.262	1.00 23.67
ATOM	1904	CB	LYS	A	300	23.576	10.154	5.403	1.00 28.77
ATOM	1905	CG	LYS	A	300	23.788	9.660	3.990	1.00 33.37
ATOM	1906	CD	LYS	A	300	22.661	8.718	3.569	1.00 38.01
ATOM	1907	CE	LYS	A	300	21.298	9.393	3.652	1.00 40.18
ATOM	1908	NZ	LYS	A	300	20.191	8.455	3.291	1.00 42.69
ATOM	1909	N	VAL	A	301	25.784	12.172	6.368	1.00 20.46
ATOM	1910	CA	VAL	A	301	26.832	13.169	6.058	1.00 18.21
ATOM	1911	C	VAL	A	301	28.083	12.842	6.867	1.00 17.93
ATOM	1912	O	VAL	A	301	29.241	12.929	6.343	1.00 16.84
ATOM	1913	CB	VAL	A	301	26.358	14.601	6.391	1.00 17.29
ATOM	1914	CG1	VAL	A	301	27.468	15.605	6.105	1.00 15.43
ATOM	1915	CG2	VAL	A	301	25.118	14.935	5.565	1.00 16.34
ATOM	1916	N	PHE	A	302	27.887	12.448	8.122	1.00 17.43
ATOM	1917	CA	PHE	A	302	29.032	12.099	8.990	1.00 18.16
ATOM	1918	C	PHE	A	302	29.854	10.957	8.399	1.00 18.95

ATOM	1919	O	PHE	A	302	31.121	11.004	8.399	1.00	18.60
ATOM	1920	CB	PHE	A	302	28.550	11.713	10.391	1.00	17.38
ATOM	1921	CG	PHE	A	302	29.639	11.180	11.265	1.00	19.16
ATOM	1922	CD1	PHE	A	302	29.866	9.810	11.362	1.00	17.81
ATOM	1923	CD2	PHE	A	302	30.498	12.051	11.923	1.00	18.89
ATOM	1924	CE1	PHE	A	302	30.934	9.320	12.096	1.00	19.63
ATOM	1925	CE2	PHE	A	302	31.573	11.569	12.660	1.00	19.90
ATOM	1926	CZ	PHE	A	302	31.793	10.201	12.747	1.00	19.13
ATOM	1927	N	GLU	A	303	29.172	9.931	7.901	1.00	19.20
ATOM	1928	CA	GLU	A	303	29.859	8.769	7.295	1.00	21.56
ATOM	1929	C	GLU	A	303	30.679	9.189	6.083	1.00	19.19
ATOM	1930	O	GLU	A	303	31.865	8.777	5.929	1.00	18.04
ATOM	1931	CB	GLU	A	303	28.836	7.704	6.888	1.00	24.72
ATOM	1932	CG	GLU	A	303	28.246	6.939	8.069	1.00	29.90
ATOM	1933	CD	GLU	A	303	27.051	6.076	7.683	1.00	33.77
ATOM	1934	OE1	GLU	A	303	26.585	5.294	8.541	1.00	36.31
ATOM	1935	OE2	GLU	A	303	26.572	6.183	6.528	1.00	36.51
ATOM	1936	N	ALA	A	304	30.088	9.998	5.216	1.00	17.86
ATOM	1937	CA	ALA	A	304	30.805	10.472	4.007	1.00	18.11
ATOM	1938	C	ALA	A	304	31.999	11.354	4.386	1.00	17.49
ATOM	1939	O	ALA	A	304	33.102	11.242	3.777	1.00	17.76
ATOM	1940	CB	ALA	A	304	29.849	11.244	3.102	1.00	17.14
ATOM	1941	N	ALA	A	305	31.812	12.221	5.377	1.00	17.06
ATOM	1942	CA	ALA	A	305	32.900	13.128	5.829	1.00	16.43
ATOM	1943	C	ALA	A	305	34.092	12.387	6.440	1.00	16.39
ATOM	1944	O	ALA	A	305	35.272	12.644	6.054	1.00	17.78
ATOM	1945	CB	ALA	A	305	32.351	14.140	6.833	1.00	15.92
ATOM	1946	N	VAL	A	306	33.842	11.476	7.375	1.00	15.50
ATOM	1947	CA	VAL	A	306	34.971	10.756	8.004	1.00	17.31
ATOM	1948	C	VAL	A	306	35.719	9.920	6.987	1.00	16.95
ATOM	1949	O	VAL	A	306	36.983	9.829	7.029	1.00	16.21
ATOM	1950	CB	VAL	A	306	34.514	9.845	9.162	1.00	17.93
ATOM	1951	CG1	VAL	A	306	33.954	10.693	10.280	1.00	19.37
ATOM	1952	CG2	VAL	A	306	33.477	8.851	8.669	1.00	19.63
ATOM	1953	N	LYS	A	307	34.987	9.307	6.065	1.00	17.11
ATOM	1954	CA	LYS	A	307	35.641	8.488	5.032	1.00	18.39
ATOM	1955	C	LYS	A	307	36.654	9.350	4.279	1.00	17.59
ATOM	1956	O	LYS	A	307	37.848	8.959	4.107	1.00	18.09
ATOM	1957	CB	LYS	A	307	34.602	7.940	4.052	1.00	19.72
ATOM	1958	CG	LYS	A	307	35.212	7.112	2.930	1.00	24.02
ATOM	1959	CD	LYS	A	307	34.147	6.415	2.102	1.00	26.72
ATOM	1960	CE	LYS	A	307	34.779	5.505	1.058	1.00	29.36
ATOM	1961	NZ	LYS	A	307	33.745	4.869	0.193	1.00	31.68
ATOM	1962	N	SER	A	308	36.205	10.520	3.842	1.00	16.75
ATOM	1963	CA	SER	A	308	37.059	11.460	3.091	1.00	17.46
ATOM	1964	C	SER	A	308	38.198	12.000	3.953	1.00	16.11
ATOM	1965	O	SER	A	308	39.378	12.056	3.501	1.00	17.12
ATOM	1966	CB	SER	A	308	36.208	12.620	2.560	1.00	17.51
ATOM	1967	OG	SER	A	308	36.982	13.505	1.774	1.00	19.76
ATOM	1968	N	ILE	A	309	37.886	12.400	5.180	1.00	16.07
ATOM	1969	CA	ILE	A	309	38.926	12.927	6.083	1.00	14.41
ATOM	1970	C	ILE	A	309	39.945	11.831	6.378	1.00	14.93
ATOM	1971	O	ILE	A	309	41.171	12.112	6.505	1.00	14.90
ATOM	1972	CB	ILE	A	309	38.310	13.439	7.401	1.00	13.88
ATOM	1973	CG1	ILE	A	309	37.346	14.595	7.099	1.00	13.08
ATOM	1974	CG2	ILE	A	309	39.404	13.887	8.350	1.00	11.40
ATOM	1975	CD1	ILE	A	309	36.575	15.084	8.315	1.00	12.70
ATOM	1976	N	LYS	A	310	39.475	10.592	6.485	1.00	15.62
ATOM	1977	CA	LYS	A	310	40.375	9.437	6.752	1.00	17.74
ATOM	1978	C	LYS	A	310	41.289	9.223	5.559	1.00	17.22
ATOM	1979	O	LYS	A	310	42.532	9.061	5.715	1.00	16.87
ATOM	1980	CB	LYS	A	310	39.577	8.149	6.976	1.00	18.35

ATOM	1981	CG	LYS	A	310	39.003	7.953	8.373	1.00 20.85
ATOM	1982	CD	LYS	A	310	38.269	6.617	8.432	1.00 22.02
ATOM	1983	CE	LYS	A	310	37.584	6.404	9.757	1.00 25.26
ATOM	1984	NZ	LYS	A	310	36.808	5.129	9.752	1.00 26.15
ATOM	1985	N	ALA	A	311	40.698	9.211	4.370	1.00 15.56
ATOM	1986	CA	ALA	A	311	41.466	9.007	3.124	1.00 17.77
ATOM	1987	C	ALA	A	311	42.549	10.071	2.990	1.00 17.36
ATOM	1988	O	ALA	A	311	43.708	9.768	2.578	1.00 20.71
ATOM	1989	CB	ALA	A	311	40.524	9.047	1.908	1.00 14.11
ATOM	1990	N	ALA	A	312	42.210	11.309	3.330	1.00 16.63
ATOM	1991	CA	ALA	A	312	43.184	12.418	3.235	1.00 15.73
ATOM	1992	C	ALA	A	312	44.247	12.342	4.333	1.00 15.59
ATOM	1993	O	ALA	A	312	45.348	12.958	4.207	1.00 13.09
ATOM	1994	CB	ALA	A	312	42.449	13.758	3.301	1.00 13.50
ATOM	1995	N	SER	A	313	43.950	11.593	5.393	1.00 17.05
ATOM	1996	CA	SER	A	313	44.867	11.432	6.560	1.00 19.05
ATOM	1997	C	SER	A	313	45.579	10.085	6.593	1.00 19.49
ATOM	1998	O	SER	A	313	46.332	9.787	7.568	1.00 21.95
ATOM	1999	CB	SER	A	313	44.075	11.555	7.865	1.00 17.23
ATOM	2000	OG	SER	A	313	43.501	12.834	8.003	1.00 23.58
ATOM	2001	N	SER	A	314	45.368	9.270	5.570	1.00 20.76
ATOM	2002	CA	SER	A	314	45.952	7.909	5.513	1.00 22.73
ATOM	2003	C	SER	A	314	47.436	7.725	5.838	1.00 21.90
ATOM	2004	O	SER	A	314	47.825	6.639	6.359	1.00 20.76
ATOM	2005	CB	SER	A	314	45.650	7.271	4.150	1.00 22.50
ATOM	2006	OG	SER	A	314	46.207	8.032	3.093	1.00 27.94
ATOM	2007	N	THR	A	315	48.285	8.714	5.570	1.00 20.90
ATOM	2008	CA	THR	A	315	49.732	8.523	5.868	1.00 23.78
ATOM	2009	C	THR	A	315	50.020	8.454	7.361	1.00 25.42
ATOM	2010	O	THR	A	315	51.191	8.219	7.784	1.00 26.24
ATOM	2011	CB	THR	A	315	50.616	9.634	5.257	1.00 23.59
ATOM	2012	OG1	THR	A	315	50.256	10.901	5.818	1.00 22.73
ATOM	2013	CG2	THR	A	315	50.456	9.668	3.745	1.00 22.59
ATOM	2014	N	GLU	A	316	48.994	8.655	8.176	1.00 27.46
ATOM	2015	CA	GLU	A	316	49.170	8.589	9.638	1.00 29.81
ATOM	2016	C	GLU	A	316	48.258	7.503	10.201	1.00 30.55
ATOM	2017	O	GLU	A	316	47.110	7.314	9.710	1.00 29.51
ATOM	2018	CB	GLU	A	316	48.819	9.931	10.279	1.00 32.51
ATOM	2019	CG	GLU	A	316	49.277	10.039	11.725	1.00 36.72
ATOM	2020	CD	GLU	A	316	50.571	10.818	11.879	1.00 36.99
ATOM	2021	OE1	GLU	A	316	51.456	10.728	11.003	1.00 37.39
ATOM	2022	OE2	GLU	A	316	50.704	11.522	12.893	1.00 41.14
ATOM	2023	N	LYS	A	317	48.736	6.775	11.205	1.00 32.69
ATOM	2024	CA	LYS	A	317	47.928	5.702	11.828	1.00 35.09
ATOM	2025	C	LYS	A	317	47.216	6.223	13.071	1.00 33.44
ATOM	2026	O	LYS	A	317	47.804	7.005	13.883	1.00 34.13
ATOM	2027	CB	LYS	A	317	48.809	4.505	12.202	1.00 38.52
ATOM	2028	CG	LYS	A	317	49.980	4.844	13.106	1.00 43.41
ATOM	2029	CD	LYS	A	317	50.665	3.588	13.638	1.00 46.99
ATOM	2030	CE	LYS	A	317	51.165	2.686	12.514	1.00 48.65
ATOM	2031	NZ	LYS	A	317	51.731	1.410	13.043	1.00 49.49
ATOM	2032	N	PHE	A	318	45.965	5.818	13.245	1.00 31.00
ATOM	2033	CA	PHE	A	318	45.188	6.272	14.408	1.00 30.33
ATOM	2034	C	PHE	A	318	44.683	5.120	15.263	1.00 30.57
ATOM	2035	O	PHE	A	318	44.171	4.088	14.732	1.00 29.80
ATOM	2036	CB	PHE	A	318	44.014	7.135	13.944	1.00 28.83
ATOM	2037	CG	PHE	A	318	44.436	8.367	13.197	1.00 28.31
ATOM	2038	CD1	PHE	A	318	44.625	8.333	11.817	1.00 27.09
ATOM	2039	CD2	PHE	A	318	44.686	9.554	13.879	1.00 27.59
ATOM	2040	CE1	PHE	A	318	45.060	9.466	11.130	1.00 27.37
ATOM	2041	CE2	PHE	A	318	45.122	10.691	13.200	1.00 26.98
ATOM	2042	CZ	PHE	A	318	45.309	10.648	11.826	1.00 27.12

ATOM	2043	N	PRO	A	319	44.805	5.252	16.591	1.00	30.02
ATOM	2044	CA	PRO	A	319	44.361	4.222	17.535	1.00	30.20
ATOM	2045	C	PRO	A	319	42.864	3.977	17.460	1.00	29.88
ATOM	2046	O	PRO	A	319	42.087	4.882	17.040	1.00	29.27
ATOM	2047	CB	PRO	A	319	44.777	4.793	18.890	1.00	30.49
ATOM	2048	CG	PRO	A	319	44.667	6.276	18.674	1.00	31.99
ATOM	2049	CD	PRO	A	319	45.308	6.437	17.309	1.00	30.77
ATOM	2050	N	ASP	A	320	42.449	2.779	17.860	1.00	30.08
ATOM	2051	CA	ASP	A	320	41.018	2.389	17.867	1.00	29.79
ATOM	2052	C	ASP	A	320	40.183	3.406	18.652	1.00	28.71
ATOM	2053	O	ASP	A	320	40.560	3.804	19.804	1.00	27.90
ATOM	2054	CB	ASP	A	320	40.855	1.009	18.520	1.00	31.81
ATOM	2055	CG	ASP	A	320	41.545	-0.104	17.740	1.00	34.27
ATOM	2056	OD1	ASP	A	320	41.787	-1.182	18.331	1.00	34.13
ATOM	2057	OD2	ASP	A	320	41.833	0.092	16.538	1.00	35.41
ATOM	2058	N	GLY	A	321	39.067	3.837	18.068	1.00	26.34
ATOM	2059	CA	GLY	A	321	38.193	4.781	18.745	1.00	24.91
ATOM	2060	C	GLY	A	321	38.439	6.259	18.490	1.00	23.96
ATOM	2061	O	GLY	A	321	37.632	7.129	18.941	1.00	23.66
ATOM	2062	N	PHE	A	322	39.519	6.591	17.793	1.00	22.07
ATOM	2063	CA	PHE	A	322	39.810	8.011	17.507	1.00	20.41
ATOM	2064	C	PHE	A	322	38.705	8.670	16.684	1.00	20.53
ATOM	2065	O	PHE	A	322	38.157	9.743	17.078	1.00	20.75
ATOM	2066	CB	PHE	A	322	41.126	8.157	16.747	1.00	19.07
ATOM	2067	CG	PHE	A	322	41.405	9.567	16.306	1.00	19.05
ATOM	2068	CD1	PHE	A	322	41.701	10.555	17.240	1.00	17.04
ATOM	2069	CD2	PHE	A	322	41.326	9.918	14.960	1.00	17.20
ATOM	2070	CE1	PHE	A	322	41.912	11.872	16.840	1.00	18.99
ATOM	2071	CE2	PHE	A	322	41.535	11.229	14.552	1.00	17.99
ATOM	2072	CZ	PHE	A	322	41.829	12.210	15.494	1.00	16.28
ATOM	2073	N	TRP	A	323	38.367	8.063	15.552	1.00	20.75
ATOM	2074	CA	TRP	A	323	37.330	8.622	14.664	1.00	22.37
ATOM	2075	C	TRP	A	323	35.940	8.626	15.273	1.00	23.50
ATOM	2076	O	TRP	A	323	35.036	9.379	14.804	1.00	22.84
ATOM	2077	CB	TRP	A	323	37.322	7.872	13.335	1.00	21.45
ATOM	2078	CG	TRP	A	323	38.643	7.924	12.664	1.00	20.71
ATOM	2079	CD1	TRP	A	323	39.566	6.921	12.594	1.00	20.50
ATOM	2080	CD2	TRP	A	323	39.217	9.049	11.986	1.00	20.31
ATOM	2081	NE1	TRP	A	323	40.679	7.349	11.913	1.00	20.18
ATOM	2082	CE2	TRP	A	323	40.492	8.651	11.527	1.00	20.95
ATOM	2083	CE3	TRP	A	323	38.778	10.354	11.722	1.00	20.80
ATOM	2084	CZ2	TRP	A	323	41.337	9.511	10.816	1.00	20.49
ATOM	2085	CZ3	TRP	A	323	39.618	11.212	11.013	1.00	21.58
ATOM	2086	CH2	TRP	A	323	40.885	10.784	10.569	1.00	21.15
ATOM	2087	N	LEU	A	324	35.734	7.810	16.300	1.00	26.13
ATOM	2088	CA	LEU	A	324	34.428	7.772	16.983	1.00	27.96
ATOM	2089	C	LEU	A	324	34.417	8.877	18.040	1.00	29.09
ATOM	2090	O	LEU	A	324	33.413	9.044	18.799	1.00	29.23
ATOM	2091	CB	LEU	A	324	34.202	6.408	17.642	1.00	29.11
ATOM	2092	CG	LEU	A	324	33.910	5.236	16.697	1.00	30.04
ATOM	2093	CD1	LEU	A	324	33.791	3.948	17.501	1.00	30.31
ATOM	2094	CD2	LEU	A	324	32.625	5.499	15.924	1.00	29.47
ATOM	2095	N	GLY	A	325	35.513	9.634	18.098	1.00	29.34
ATOM	2096	CA	GLY	A	325	35.632	10.728	19.048	1.00	30.68
ATOM	2097	C	GLY	A	325	35.794	10.280	20.489	1.00	31.19
ATOM	2098	O	GLY	A	325	35.687	11.109	21.442	1.00	31.53
ATOM	2099	N	GLU	A	326	36.067	8.995	20.683	1.00	32.22
ATOM	2100	CA	GLU	A	326	36.225	8.436	22.042	1.00	34.09
ATOM	2101	C	GLU	A	326	37.655	8.482	22.563	1.00	33.56
ATOM	2102	O	GLU	A	326	37.907	8.933	23.720	1.00	34.19
ATOM	2103	CB	GLU	A	326	35.728	6.992	22.062	1.00	35.56
ATOM	2104	CG	GLU	A	326	34.267	6.847	21.683	1.00	38.03

ATOM	2105	CD	GLU	A	326	33.855	5.401	21.494	1.00	40.36
ATOM	2106	OE1	GLU	A	326	32.662	5.162	21.207	1.00	41.84
ATOM	2107	OE2	GLU	A	326	34.720	4.506	21.626	1.00	42.10
ATOM	2108	N	GLN	A	327	38.602	8.031	21.750	1.00	32.81
ATOM	2109	CA	GLN	A	327	40.009	8.017	22.178	1.00	31.36
ATOM	2110	C	GLN	A	327	40.844	9.142	21.608	1.00	30.14
ATOM	2111	O	GLN	A	327	40.612	9.626	20.458	1.00	28.97
ATOM	2112	CB	GLN	A	327	40.650	6.667	21.842	1.00	34.41
ATOM	2113	CG	GLN	A	327	40.770	5.749	23.060	1.00	38.96
ATOM	2114	CD	GLN	A	327	39.443	5.546	23.778	1.00	40.61
ATOM	2115	OE1	GLN	A	327	39.410	5.223	25.002	1.00	42.73
ATOM	2116	NE2	GLN	A	327	38.344	5.714	23.053	1.00	42.75
ATOM	2117	N	LEU	A	328	41.814	9.581	22.394	1.00	28.01
ATOM	2118	CA	LEU	A	328	42.695	10.663	21.964	1.00	28.64
ATOM	2119	C	LEU	A	328	43.889	10.100	21.219	1.00	27.50
ATOM	2120	O	LEU	A	328	44.207	8.873	21.317	1.00	27.23
ATOM	2121	CB	LEU	A	328	43.177	11.467	23.180	1.00	29.39
ATOM	2122	CG	LEU	A	328	43.924	10.735	24.304	1.00	31.09
ATOM	2123	CD1	LEU	A	328	45.298	10.283	23.831	1.00	31.75
ATOM	2124	CD2	LEU	A	328	44.074	11.669	25.498	1.00	31.12
ATOM	2125	N	VAL	A	329	44.539	10.961	20.449	1.00	25.26
ATOM	2126	CA	VAL	A	329	45.748	10.583	19.722	1.00	23.64
ATOM	2127	C	VAL	A	329	46.779	11.593	20.203	1.00	23.76
ATOM	2128	O	VAL	A	329	46.431	12.786	20.476	1.00	21.96
ATOM	2129	CB	VAL	A	329	45.560	10.675	18.194	1.00	23.82
ATOM	2130	CG1	VAL	A	329	45.100	12.070	17.794	1.00	23.64
ATOM	2131	CG2	VAL	A	329	46.866	10.317	17.501	1.00	23.70
ATOM	2132	N	CYS	A	330	48.025	11.157	20.344	1.00	23.69
ATOM	2133	CA	CYS	A	330	49.088	12.046	20.830	1.00	24.17
ATOM	2134	C	CYS	A	330	50.315	12.060	19.937	1.00	23.87
ATOM	2135	O	CYS	A	330	50.592	11.089	19.165	1.00	24.32
ATOM	2136	CB	CYS	A	330	49.548	11.633	22.228	1.00	24.93
ATOM	2137	SG	CYS	A	330	48.353	11.638	23.608	1.00	29.07
ATOM	2138	N	TRP	A	331	51.069	13.144	20.047	1.00	22.66
ATOM	2139	CA	TRP	A	331	52.306	13.318	19.281	1.00	22.40
ATOM	2140	C	TRP	A	331	53.333	13.972	20.177	1.00	22.22
ATOM	2141	O	TRP	A	331	52.979	14.698	21.154	1.00	21.57
ATOM	2142	CB	TRP	A	331	52.069	14.207	18.064	1.00	21.16
ATOM	2143	CG	TRP	A	331	51.345	13.524	16.959	1.00	19.61
ATOM	2144	CD1	TRP	A	331	51.868	12.634	16.067	1.00	18.33
ATOM	2145	CD2	TRP	A	331	49.966	13.684	16.606	1.00	18.42
ATOM	2146	NE1	TRP	A	331	50.902	12.233	15.177	1.00	17.37
ATOM	2147	CE2	TRP	A	331	49.721	12.862	15.488	1.00	18.60
ATOM	2148	CE3	TRP	A	331	48.911	14.446	17.130	1.00	19.20
ATOM	2149	CZ2	TRP	A	331	48.467	12.778	14.874	1.00	17.86
ATOM	2150	CZ3	TRP	A	331	47.659	14.364	16.521	1.00	19.94
ATOM	2151	CH2	TRP	A	331	47.450	13.535	15.406	1.00	19.08
ATOM	2152	N	GLN	A	332	54.598	13.730	19.873	1.00	23.04
ATOM	2153	CA	GLN	A	332	55.689	14.321	20.648	1.00	25.14
ATOM	2154	C	GLN	A	332	55.490	15.836	20.594	1.00	23.64
ATOM	2155	O	GLN	A	332	55.066	16.397	19.533	1.00	23.11
ATOM	2156	CB	GLN	A	332	57.020	13.937	20.015	1.00	27.80
ATOM	2157	CG	GLN	A	332	58.171	13.877	20.982	1.00	33.30
ATOM	2158	CD	GLN	A	332	59.450	13.445	20.305	1.00	35.55
ATOM	2159	OE1	GLN	A	332	60.060	14.224	19.507	1.00	36.94
ATOM	2160	NE2	GLN	A	332	59.879	12.217	20.579	1.00	36.57
ATOM	2161	N	ALA	A	333	55.778	16.506	21.704	1.00	22.79
ATOM	2162	CA	ALA	A	333	55.618	17.977	21.820	1.00	21.04
ATOM	2163	C	ALA	A	333	55.936	18.759	20.552	1.00	19.77
ATOM	2164	O	ALA	A	333	57.076	18.671	19.997	1.00	19.85
ATOM	2165	CB	ALA	A	333	56.475	18.499	22.971	1.00	21.00
ATOM	2166	N	GLY	A	334	54.949	19.515	20.083	1.00	17.64

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ATOM   2167  CA  GLY A 334      55.123  20.340  18.903  1.00 16.89
ATOM   2168  C   GLY A 334      55.205  19.663  17.548  1.00 17.61
ATOM   2169  O   GLY A 334      55.403  20.370  16.512  1.00 17.50
ATOM   2170  N   THR A 335      55.060  18.343  17.490  1.00 16.55
ATOM   2171  CA  THR A 335      55.146  17.648  16.182  1.00 17.58
ATOM   2172  C   THR A 335      53.802  17.260  15.557  1.00 16.83
ATOM   2173  O   THR A 335      53.761  16.408  14.618  1.00 17.71
ATOM   2174  CB  THR A 335      56.017  16.377  16.275  1.00 17.76
ATOM   2175  OG1 THR A 335      55.361  15.401  17.095  1.00 17.56
ATOM   2176  CG2 THR A 335      57.373  16.710  16.884  1.00 17.23
ATOM   2177  N   THR A 336      52.707  17.842  16.037  1.00 16.75
ATOM   2178  CA  THR A 336      51.373  17.527  15.460  1.00 16.56
ATOM   2179  C   THR A 336      51.473  17.752  13.952  1.00 16.24
ATOM   2180  O   THR A 336      51.821  18.868  13.487  1.00 16.30
ATOM   2181  CB  THR A 336      50.267  18.437  16.030  1.00 17.05
ATOM   2182  OG1 THR A 336      50.181  18.255  17.451  1.00 17.15
ATOM   2183  CG2 THR A 336      48.917  18.096  15.401  1.00 16.72
ATOM   2184  N   PRO A 337      51.182  16.718  13.157  1.00 15.50
ATOM   2185  CA  PRO A 337      51.254  16.820  11.699  1.00 14.87
ATOM   2186  C   PRO A 337      50.006  17.444  11.082  1.00 14.56
ATOM   2187  O   PRO A 337      49.310  16.800  10.249  1.00 14.49
ATOM   2188  CB  PRO A 337      51.448  15.369  11.281  1.00 15.18
ATOM   2189  CG  PRO A 337      50.520  14.657  12.238  1.00 16.05
ATOM   2190  CD  PRO A 337      50.784  15.359  13.572  1.00 15.54
ATOM   2191  N   TRP A 338      49.713  18.682  11.470  1.00 14.89
ATOM   2192  CA  TRP A 338      48.535  19.415  10.956  1.00 14.85
ATOM   2193  C   TRP A 338      48.339  19.304   9.445  1.00 14.87
ATOM   2194  O   TRP A 338      47.194  19.048   8.966  1.00 17.13
ATOM   2195  CB  TRP A 338      48.639  20.899  11.313  1.00 13.77
ATOM   2196  CG  TRP A 338      48.784  21.176  12.767  1.00 15.11
ATOM   2197  CD1 TRP A 338      49.897  21.652  13.411  1.00 14.78
ATOM   2198  CD2 TRP A 338      47.780  21.011  13.771  1.00 14.17
ATOM   2199  NE1 TRP A 338      49.641  21.794  14.756  1.00 14.64
ATOM   2200  CE2 TRP A 338      48.348  21.407  15.003  1.00 14.35
ATOM   2201  CE3 TRP A 338      46.451  20.566  13.751  1.00 14.31
ATOM   2202  CZ2 TRP A 338      47.635  21.371  16.202  1.00 14.86
ATOM   2203  CZ3 TRP A 338      45.744  20.530  14.945  1.00 16.02
ATOM   2204  CH2 TRP A 338      46.339  20.932  16.154  1.00 14.77
ATOM   2205  N   ASN A 339      49.414  19.486   8.682  1.00 13.22
ATOM   2206  CA  ASN A 339      49.319  19.449   7.203  1.00 12.87
ATOM   2207  C   ASN A 339      48.674  18.208   6.608  1.00 12.01
ATOM   2208  O   ASN A 339      48.061  18.288   5.508  1.00 13.99
ATOM   2209  CB  ASN A 339      50.699  19.649   6.552  1.00 12.61
ATOM   2210  CG  ASN A 339      51.576  18.404   6.627  1.00 15.28
ATOM   2211  OD1 ASN A 339      52.290  18.174   7.648  1.00 16.29
ATOM   2212  ND2 ASN A 339      51.541  17.584   5.578  1.00 12.93
ATOM   2213  N   ILE A 340      48.774  17.064   7.276  1.00 12.88
ATOM   2214  CA  ILE A 340      48.171  15.831   6.698  1.00 12.98
ATOM   2215  C   ILE A 340      46.655  15.864   6.794  1.00 12.80
ATOM   2216  O   ILE A 340      45.944  15.237   5.959  1.00 12.80
ATOM   2217  CB  ILE A 340      48.667  14.545   7.400  1.00 14.79
ATOM   2218  CG1 ILE A 340      48.142  14.512   8.833  1.00 14.91
ATOM   2219  CG2 ILE A 340      50.194  14.483   7.372  1.00 12.38
ATOM   2220  CD1 ILE A 340      48.177  13.142   9.454  1.00 17.42
ATOM   2221  N   PHE A 341      46.138  16.577   7.790  1.00 13.19
ATOM   2222  CA  PHE A 341      44.677  16.689   7.972  1.00 13.87
ATOM   2223  C   PHE A 341      44.143  17.741   7.006  1.00 13.37
ATOM   2224  O   PHE A 341      44.787  18.812   6.798  1.00 12.72
ATOM   2225  CB  PHE A 341      44.354  17.087   9.410  1.00 13.10
ATOM   2226  CG  PHE A 341      44.685  16.027  10.429  1.00 13.55
ATOM   2227  CD1 PHE A 341      43.817  14.960  10.654  1.00 13.48
ATOM   2228  CD2 PHE A 341      45.861  16.104  11.171  1.00 12.12
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ATOM	2229	CE1	PHE	A	341	44.115	13.984	11.607	1.00 13.44
ATOM	2230	CE2	PHE	A	341	46.172	15.136	12.127	1.00 14.31
ATOM	2231	CZ	PHE	A	341	45.298	14.074	12.346	1.00 13.92
ATOM	2232	N	PRO	A	342	42.975	17.484	6.402	1.00 12.78
ATOM	2233	CA	PRO	A	342	42.357	18.413	5.448	1.00 12.17
ATOM	2234	C	PRO	A	342	41.565	19.544	6.100	1.00 12.90
ATOM	2235	O	PRO	A	342	41.168	19.465	7.309	1.00 12.52
ATOM	2236	CB	PRO	A	342	41.447	17.502	4.638	1.00 10.18
ATOM	2237	CG	PRO	A	342	40.920	16.570	5.714	1.00 11.48
ATOM	2238	CD	PRO	A	342	42.180	16.244	6.523	1.00 12.10
ATOM	2239	N	VAL	A	343	41.342	20.609	5.342	1.00 12.27
ATOM	2240	CA	VAL	A	343	40.528	21.712	5.851	1.00 10.51
ATOM	2241	C	VAL	A	343	39.101	21.281	5.521	1.00 12.41
ATOM	2242	O	VAL	A	343	38.878	20.401	4.632	1.00 10.45
ATOM	2243	CB	VAL	A	343	40.838	23.054	5.143	1.00 10.23
ATOM	2244	CG1	VAL	A	343	42.247	23.507	5.488	1.00 8.58
ATOM	2245	CG2	VAL	A	343	40.672	22.914	3.636	1.00 8.08
ATOM	2246	N	ILE	A	344	38.132	21.848	6.224	1.00 13.49
ATOM	2247	CA	ILE	A	344	36.725	21.507	5.991	1.00 13.17
ATOM	2248	C	ILE	A	344	35.989	22.789	5.664	1.00 13.33
ATOM	2249	O	ILE	A	344	36.067	23.795	6.427	1.00 13.12
ATOM	2250	CB	ILE	A	344	36.099	20.859	7.246	1.00 14.77
ATOM	2251	CG1	ILE	A	344	36.776	19.512	7.517	1.00 14.50
ATOM	2252	CG2	ILE	A	344	34.585	20.702	7.060	1.00 13.14
ATOM	2253	CD1	ILE	A	344	36.374	18.875	8.825	1.00 17.73
ATOM	2254	N	SER	A	345	35.292	22.794	4.537	1.00 12.41
ATOM	2255	CA	SER	A	345	34.547	23.982	4.136	1.00 13.41
ATOM	2256	C	SER	A	345	33.051	23.723	4.172	1.00 14.94
ATOM	2257	O	SER	A	345	32.555	22.641	3.721	1.00 14.55
ATOM	2258	CB	SER	A	345	34.967	24.430	2.728	1.00 14.23
ATOM	2259	OG	SER	A	345	36.329	24.834	2.703	1.00 13.57
ATOM	2260	N	LEU	A	346	32.320	24.682	4.725	1.00 13.42
ATOM	2261	CA	LEU	A	346	30.859	24.594	4.796	1.00 14.08
ATOM	2262	C	LEU	A	346	30.320	25.772	4.003	1.00 13.86
ATOM	2263	O	LEU	A	346	30.681	26.956	4.286	1.00 13.52
ATOM	2264	CB	LEU	A	346	30.383	24.674	6.252	1.00 15.83
ATOM	2265	CG	LEU	A	346	30.239	23.372	7.051	1.00 17.74
ATOM	2266	CD1	LEU	A	346	31.455	22.492	6.875	1.00 18.92
ATOM	2267	CD2	LEU	A	346	30.028	23.711	8.521	1.00 19.69
ATOM	2268	N	TYR	A	347	29.496	25.485	3.000	1.00 13.48
ATOM	2269	CA	TYR	A	347	28.894	26.543	2.176	1.00 13.76
ATOM	2270	C	TYR	A	347	27.525	26.864	2.745	1.00 14.58
ATOM	2271	O	TYR	A	347	26.676	25.948	2.979	1.00 13.16
ATOM	2272	CB	TYR	A	347	28.757	26.101	0.716	1.00 14.82
ATOM	2273	CG	TYR	A	347	30.066	26.051	-0.034	1.00 15.10
ATOM	2274	CD1	TYR	A	347	31.022	25.074	0.252	1.00 13.97
ATOM	2275	CD2	TYR	A	347	30.349	26.977	-1.038	1.00 13.98
ATOM	2276	CE1	TYR	A	347	32.228	25.018	-0.447	1.00 14.47
ATOM	2277	CE2	TYR	A	347	31.556	26.930	-1.746	1.00 15.69
ATOM	2278	CZ	TYR	A	347	32.487	25.949	-1.445	1.00 15.09
ATOM	2279	OH	TYR	A	347	33.672	25.895	-2.141	1.00 16.72
ATOM	2280	N	LEU	A	348	27.288	28.145	2.971	1.00 13.86
ATOM	2281	CA	LEU	A	348	26.018	28.593	3.545	1.00 16.70
ATOM	2282	C	LEU	A	348	25.246	29.445	2.559	1.00 17.37
ATOM	2283	O	LEU	A	348	25.856	30.183	1.722	1.00 16.05
ATOM	2284	CB	LEU	A	348	26.292	29.401	4.814	1.00 15.57
ATOM	2285	CG	LEU	A	348	27.019	28.620	5.908	1.00 17.10
ATOM	2286	CD1	LEU	A	348	27.518	29.565	6.985	1.00 15.71
ATOM	2287	CD2	LEU	A	348	26.078	27.580	6.495	1.00 16.92
ATOM	2288	N	MET	A	349	23.922	29.352	2.617	1.00 19.68
ATOM	2289	CA	MET	A	349	23.073	30.167	1.734	1.00 22.78
ATOM	2290	C	MET	A	349	23.384	31.629	2.024	1.00 22.03

ATOM	2291	O	MET	A	349	23.478	32.049	3.222	1.00	20.70
ATOM	2292	CB	MET	A	349	21.594	29.897	2.008	1.00	25.40
ATOM	2293	CG	MET	A	349	20.931	28.954	1.012	1.00	31.18
ATOM	2294	SD	MET	A	349	19.139	28.833	1.272	1.00	37.43
ATOM	2295	CE	MET	A	349	18.697	30.583	1.318	1.00	32.73
ATOM	2296	N	GLY	A	350	23.573	32.414	0.972	1.00	20.81
ATOM	2297	CA	GLY	A	350	23.857	33.824	1.167	1.00	23.50
ATOM	2298	C	GLY	A	350	22.565	34.612	1.280	1.00	24.26
ATOM	2299	O	GLY	A	350	21.450	34.042	1.091	1.00	23.13
ATOM	2300	N	GLU	A	351	22.662	35.899	1.591	1.00	27.25
ATOM	2301	CA	GLU	A	351	21.448	36.734	1.698	1.00	32.00
ATOM	2302	C	GLU	A	351	20.870	36.948	0.306	1.00	33.92
ATOM	2303	O	GLU	A	351	19.620	37.066	0.125	1.00	34.42
ATOM	2304	CB	GLU	A	351	21.774	38.081	2.340	1.00	32.31
ATOM	2305	CG	GLU	A	351	22.012	37.996	3.831	1.00	34.92
ATOM	2306	CD	GLU	A	351	21.916	39.346	4.503	1.00	35.55
ATOM	2307	OE1	GLU	A	351	22.819	40.187	4.293	1.00	36.64
ATOM	2308	OE2	GLU	A	351	20.927	39.567	5.233	1.00	36.29
ATOM	2309	N	VAL	A	352	21.753	37.007	-0.684	1.00	36.98
ATOM	2310	CA	VAL	A	352	21.327	37.181	-2.082	1.00	38.72
ATOM	2311	C	VAL	A	352	20.944	35.809	-2.629	1.00	40.47
ATOM	2312	O	VAL	A	352	21.689	34.799	-2.426	1.00	39.68
ATOM	2313	CB	VAL	A	352	22.456	37.767	-2.939	1.00	38.31
ATOM	2314	CG1	VAL	A	352	21.999	37.892	-4.382	1.00	38.33
ATOM	2315	CG2	VAL	A	352	22.866	39.123	-2.391	1.00	37.93
ATOM	2316	N	THR	A	353	19.806	35.747	-3.314	1.00	42.33
ATOM	2317	CA	THR	A	353	19.300	34.476	-3.882	1.00	43.97
ATOM	2318	C	THR	A	353	20.254	33.832	-4.877	1.00	43.18
ATOM	2319	O	THR	A	353	20.941	34.536	-5.688	1.00	42.65
ATOM	2320	CB	THR	A	353	17.929	34.672	-4.578	1.00	45.29
ATOM	2321	OG1	THR	A	353	18.018	35.743	-5.526	1.00	46.63
ATOM	2322	CG2	THR	A	353	16.849	34.988	-3.551	1.00	46.31
ATOM	2323	N	ASN	A	354	20.307	32.507	-4.839	1.00	42.20
ATOM	2324	CA	ASN	A	354	21.183	31.741	-5.742	1.00	43.39
ATOM	2325	C	ASN	A	354	22.641	32.166	-5.611	1.00	41.22
ATOM	2326	O	ASN	A	354	23.444	32.078	-6.584	1.00	43.04
ATOM	2327	CB	ASN	A	354	20.698	31.887	-7.187	1.00	45.64
ATOM	2328	CG	ASN	A	354	19.467	31.036	-7.474	1.00	47.44
ATOM	2329	OD1	ASN	A	354	18.824	31.163	-8.562	1.00	48.61
ATOM	2330	ND2	ASN	A	354	19.121	30.159	-6.534	1.00	47.73
ATOM	2331	N	GLN	A	355	22.999	32.621	-4.419	1.00	37.62
ATOM	2332	CA	GLN	A	355	24.371	33.042	-4.128	1.00	34.85
ATOM	2333	C	GLN	A	355	24.737	32.475	-2.764	1.00	32.57
ATOM	2334	O	GLN	A	355	23.863	32.388	-1.846	1.00	31.25
ATOM	2335	CB	GLN	A	355	24.459	34.563	-4.105	1.00	35.77
ATOM	2336	CG	GLN	A	355	25.834	35.089	-3.797	1.00	38.04
ATOM	2337	CD	GLN	A	355	25.909	36.590	-3.915	1.00	39.05
ATOM	2338	OE1	GLN	A	355	25.586	37.171	-4.992	1.00	40.57
ATOM	2339	NE2	GLN	A	355	26.331	37.249	-2.844	1.00	39.68
ATOM	2340	N	SER	A	356	25.989	32.071	-2.597	1.00	29.33
ATOM	2341	CA	SER	A	356	26.419	31.514	-1.304	1.00	25.60
ATOM	2342	C	SER	A	356	27.850	31.897	-0.981	1.00	22.66
ATOM	2343	O	SER	A	356	28.580	32.481	-1.833	1.00	21.99
ATOM	2344	CB	SER	A	356	26.313	29.991	-1.318	1.00	25.71
ATOM	2345	OG	SER	A	356	27.449	29.425	-1.945	1.00	24.59
ATOM	2346	N	PHE	A	357	28.267	31.583	0.239	1.00	20.53
ATOM	2347	CA	PHE	A	357	29.639	31.865	0.676	1.00	17.95
ATOM	2348	C	PHE	A	357	30.104	30.643	1.437	1.00	17.15
ATOM	2349	O	PHE	A	357	29.279	29.750	1.784	1.00	17.21
ATOM	2350	CB	PHE	A	357	29.687	33.126	1.550	1.00	17.62
ATOM	2351	CG	PHE	A	357	28.926	33.017	2.850	1.00	17.61
ATOM	2352	CD1	PHE	A	357	29.571	32.625	4.018	1.00	15.09

ATOM	2353	CD2	PHE	A	357	27.577	33.357	2.912	1.00	16.90
ATOM	2354	CE1	PHE	A	357	28.887	32.577	5.229	1.00	14.87
ATOM	2355	CE2	PHE	A	357	26.881	33.312	4.120	1.00	15.64
ATOM	2356	CZ	PHE	A	357	27.538	32.924	5.280	1.00	16.14
ATOM	2357	N	ARG	A	358	31.397	30.545	1.687	1.00	16.29
ATOM	2358	CA	ARG	A	358	31.891	29.383	2.412	1.00	14.04
ATOM	2359	C	ARG	A	358	32.642	29.755	3.664	1.00	14.59
ATOM	2360	O	ARG	A	358	33.237	30.869	3.785	1.00	13.01
ATOM	2361	CB	ARG	A	358	32.784	28.525	1.516	1.00	14.11
ATOM	2362	CG	ARG	A	358	34.084	29.172	1.102	1.00	13.28
ATOM	2363	CD	ARG	A	358	34.809	28.275	0.121	1.00	13.06
ATOM	2364	NE	ARG	A	358	36.090	28.831	-0.291	1.00	14.39
ATOM	2365	CZ	ARG	A	358	36.723	28.489	-1.409	1.00	14.92
ATOM	2366	NH1	ARG	A	358	36.188	27.591	-2.232	1.00	13.71
ATOM	2367	NH2	ARG	A	358	37.888	29.045	-1.701	1.00	12.88
ATOM	2368	N	ILE	A	359	32.612	28.819	4.596	1.00	14.51
ATOM	2369	CA	ILE	A	359	33.268	28.935	5.891	1.00	16.36
ATOM	2370	C	ILE	A	359	34.242	27.762	5.913	1.00	15.41
ATOM	2371	O	ILE	A	359	33.836	26.583	5.675	1.00	15.49
ATOM	2372	CB	ILE	A	359	32.197	28.824	7.001	1.00	17.94
ATOM	2373	CG1	ILE	A	359	31.543	30.190	7.198	1.00	19.68
ATOM	2374	CG2	ILE	A	359	32.766	28.260	8.255	1.00	20.12
ATOM	2375	CD1	ILE	A	359	32.515	31.288	7.500	1.00	22.40
ATOM	2376	N	THR	A	360	35.513	28.046	6.162	1.00	13.01
ATOM	2377	CA	THR	A	360	36.531	26.983	6.167	1.00	14.32
ATOM	2378	C	THR	A	360	37.307	26.894	7.470	1.00	14.04
ATOM	2379	O	THR	A	360	37.892	27.913	7.938	1.00	13.82
ATOM	2380	CB	THR	A	360	37.536	27.202	5.021	1.00	14.49
ATOM	2381	OG1	THR	A	360	36.828	27.286	3.774	1.00	15.69
ATOM	2382	CG2	THR	A	360	38.532	26.053	4.964	1.00	15.11
ATOM	2383	N	ILE	A	361	37.331	25.709	8.074	1.00	13.79
ATOM	2384	CA	ILE	A	361	38.091	25.524	9.330	1.00	17.36
ATOM	2385	C	ILE	A	361	39.241	24.548	9.122	1.00	16.53
ATOM	2386	O	ILE	A	361	39.237	23.717	8.160	1.00	16.37
ATOM	2387	CB	ILE	A	361	37.208	24.982	10.476	1.00	18.15
ATOM	2388	CG1	ILE	A	361	36.608	23.632	10.077	1.00	18.53
ATOM	2389	CG2	ILE	A	361	36.126	25.999	10.830	1.00	18.95
ATOM	2390	CD1	ILE	A	361	35.899	22.937	11.208	1.00	18.19
ATOM	2391	N	LEU	A	362	40.230	24.614	9.998	1.00	17.82
ATOM	2392	CA	LEU	A	362	41.375	23.710	9.876	1.00	18.92
ATOM	2393	C	LEU	A	362	41.412	22.659	10.983	1.00	17.87
ATOM	2394	O	LEU	A	362	40.533	22.654	11.912	1.00	17.21
ATOM	2395	CB	LEU	A	362	42.675	24.525	9.837	1.00	22.47
ATOM	2396	CG	LEU	A	362	42.686	25.974	10.320	1.00	25.03
ATOM	2397	CD1	LEU	A	362	42.945	25.992	11.802	1.00	28.14
ATOM	2398	CD2	LEU	A	362	43.781	26.751	9.623	1.00	25.06
ATOM	2399	N	PRO	A	363	42.380	21.729	10.910	1.00	16.12
ATOM	2400	CA	PRO	A	363	42.507	20.681	11.925	1.00	14.51
ATOM	2401	C	PRO	A	363	42.628	21.325	13.303	1.00	14.50
ATOM	2402	O	PRO	A	363	42.234	20.710	14.339	1.00	13.48
ATOM	2403	CB	PRO	A	363	43.801	19.971	11.534	1.00	15.57
ATOM	2404	CG	PRO	A	363	43.902	20.202	10.076	1.00	16.87
ATOM	2405	CD	PRO	A	363	43.450	21.616	9.903	1.00	14.60
ATOM	2406	N	GLN	A	364	43.178	22.539	13.337	1.00	12.36
ATOM	2407	CA	GLN	A	364	43.357	23.271	14.608	1.00	13.04
ATOM	2408	C	GLN	A	364	42.014	23.557	15.254	1.00	13.41
ATOM	2409	O	GLN	A	364	41.953	23.895	16.467	1.00	12.73
ATOM	2410	CB	GLN	A	364	44.111	24.585	14.392	1.00	12.04
ATOM	2411	CG	GLN	A	364	45.637	24.449	14.304	1.00	11.85
ATOM	2412	CD	GLN	A	364	46.141	24.079	12.919	1.00	11.11
ATOM	2413	OE1	GLN	A	364	47.372	24.211	12.625	1.00	13.65
ATOM	2414	NE2	GLN	A	364	45.245	23.621	12.056	1.00	8.04

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ATOM   2415  N   GLN A 365      40.939  23.446  14.478  1.00 13.30
ATOM   2416  CA  GLN A 365      39.580  23.657  15.023  1.00 14.36
ATOM   2417  C   GLN A 365      38.873  22.341  15.339  1.00 14.57
ATOM   2418  O   GLN A 365      38.312  22.175  16.457  1.00 16.56
ATOM   2419  CB  GLN A 365      38.691  24.452  14.056  1.00 14.03
ATOM   2420  CG  GLN A 365      38.816  25.962  14.167  1.00 15.23
ATOM   2421  CD  GLN A 365      40.073  26.489  13.515  1.00 15.81
ATOM   2422  OE1 GLN A 365      40.290  26.292  12.282  1.00 15.51
ATOM   2423  NE2 GLN A 365      40.917  27.158  14.295  1.00 15.82
ATOM   2424  N   TYR A 366      38.873  21.392  14.406  1.00 14.93
ATOM   2425  CA  TYR A 366      38.149  20.128  14.673  1.00 15.12
ATOM   2426  C   TYR A 366      38.914  19.053  15.447  1.00 15.66
ATOM   2427  O   TYR A 366      38.378  17.930  15.703  1.00 17.42
ATOM   2428  CB  TYR A 366      37.557  19.567  13.371  1.00 14.28
ATOM   2429  CG  TYR A 366      38.541  19.107  12.322  1.00 13.05
ATOM   2430  CD1 TYR A 366      39.228  17.907  12.467  1.00 13.67
ATOM   2431  CD2 TYR A 366      38.721  19.835  11.145  1.00 13.44
ATOM   2432  CE1 TYR A 366      40.062  17.431  11.463  1.00 12.91
ATOM   2433  CE2 TYR A 366      39.555  19.369  10.128  1.00 12.63
ATOM   2434  CZ  TYR A 366      40.218  18.163  10.294  1.00 13.86
ATOM   2435  OH  TYR A 366      41.008  17.669   9.287  1.00 12.42
ATOM   2436  N   LEU A 367      40.144  19.367  15.835  1.00 16.84
ATOM   2437  CA  LEU A 367      40.966  18.450  16.660  1.00 16.98
ATOM   2438  C   LEU A 367      40.996  19.161  18.017  1.00 17.50
ATOM   2439  O   LEU A 367      41.662  20.224  18.172  1.00 16.40
ATOM   2440  CB  LEU A 367      42.382  18.324  16.088  1.00 17.44
ATOM   2441  CG  LEU A 367      42.764  16.991  15.429  1.00 18.54
ATOM   2442  CD1 LEU A 367      41.681  16.534  14.482  1.00 17.60
ATOM   2443  CD2 LEU A 367      44.091  17.143  14.700  1.00 17.38
ATOM   2444  N   ARG A 368      40.270  18.624  18.990  1.00 17.06
ATOM   2445  CA  ARG A 368      40.192  19.253  20.326  1.00 17.22
ATOM   2446  C   ARG A 368      41.341  18.874  21.243  1.00 16.52
ATOM   2447  O   ARG A 368      41.554  17.662  21.538  1.00 16.19
ATOM   2448  CB  ARG A 368      38.879  18.871  21.009  1.00 16.02
ATOM   2449  CG  ARG A 368      38.050  20.055  21.444  1.00 19.09
ATOM   2450  CD  ARG A 368      37.415  19.811  22.792  1.00 17.88
ATOM   2451  NE  ARG A 368      36.840  18.474  22.906  1.00 17.20
ATOM   2452  CZ  ARG A 368      36.775  17.806  24.053  1.00 18.65
ATOM   2453  NH1 ARG A 368      37.247  18.361  25.164  1.00 18.77
ATOM   2454  NH2 ARG A 368      36.258  16.584  24.095  1.00 17.53
ATOM   2455  N   PRO A 369      42.100  19.867  21.722  1.00 17.88
ATOM   2456  CA  PRO A 369      43.220  19.558  22.615  1.00 19.69
ATOM   2457  C   PRO A 369      42.744  19.067  23.969  1.00 22.16
ATOM   2458  O   PRO A 369      41.786  19.645  24.575  1.00 20.49
ATOM   2459  CB  PRO A 369      43.983  20.883  22.700  1.00 20.03
ATOM   2460  CG  PRO A 369      42.932  21.911  22.429  1.00 19.96
ATOM   2461  CD  PRO A 369      42.122  21.285  21.320  1.00 17.42
ATOM   2462  N   VAL A 370      43.376  18.001  24.444  1.00 23.75
ATOM   2463  CA  VAL A 370      43.040  17.399  25.747  1.00 27.84
ATOM   2464  C   VAL A 370      44.332  16.921  26.394  1.00 30.26
ATOM   2465  O   VAL A 370      45.321  16.577  25.682  1.00 30.79
ATOM   2466  CB  VAL A 370      42.093  16.197  25.577  1.00 26.52
ATOM   2467  CG1 VAL A 370      40.771  16.654  24.989  1.00 26.57
ATOM   2468  CG2 VAL A 370      42.737  15.160  24.669  1.00 26.53
ATOM   2469  N   GLU A 371      44.361  16.891  27.719  1.00 35.50
ATOM   2470  CA  GLU A 371      45.574  16.450  28.426  1.00 40.60
ATOM   2471  C   GLU A 371      45.800  14.963  28.235  1.00 42.42
ATOM   2472  O   GLU A 371      44.832  14.138  28.321  1.00 41.89
ATOM   2473  CB  GLU A 371      45.472  16.758  29.921  1.00 43.12
ATOM   2474  CG  GLU A 371      46.603  17.634  30.443  1.00 47.33
ATOM   2475  CD  GLU A 371      47.954  17.245  29.864  1.00 49.98
ATOM   2476  OE1 GLU A 371      48.264  16.036  29.818  1.00 51.63
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ATOM   2477  OE2 GLU A 371      48.710  18.151  29.456  1.00 51.00
ATOM   2478  N   ASP A 372      47.046  14.596  27.960  1.00 45.77
ATOM   2479  CA  ASP A 372      47.396  13.182  27.774  1.00 49.75
ATOM   2480  C   ASP A 372      46.889  12.468  29.014  1.00 52.41
ATOM   2481  O   ASP A 372      47.090  12.966  30.165  1.00 52.32
ATOM   2482  CB  ASP A 372      48.913  13.015  27.665  1.00 50.28
ATOM   2483  CG  ASP A 372      49.323  11.587  27.333  1.00 51.15
ATOM   2484  OD1 ASP A 372      50.541  11.323  27.246  1.00 51.32
ATOM   2485  OD2 ASP A 372      48.429  10.729  27.156  1.00 50.76
ATOM   2486  N   VAL A 373      46.217  11.340  28.819  1.00 55.35
ATOM   2487  CA  VAL A 373      45.688  10.570  29.956  1.00 58.73
ATOM   2488  C   VAL A 373      46.850  10.213  30.896  1.00 60.04
ATOM   2489  O   VAL A 373      47.465   9.105  30.817  1.00 60.06
ATOM   2490  CB  VAL A 373      44.901   9.313  29.433  1.00 59.43
ATOM   2491  CG1 VAL A 373      45.292   8.044  30.176  1.00 59.64
ATOM   2492  CG2 VAL A 373      43.402   9.556  29.597  1.00 59.89
ATOM   2493  N   ALA A 374      47.187  11.169  31.759  1.00 61.58
ATOM   2494  CA  ALA A 374      48.277  11.020  32.755  1.00 61.52
ATOM   2495  C   ALA A 374      49.709  11.205  32.233  1.00 61.38
ATOM   2496  O   ALA A 374      50.104  10.633  31.169  1.00 60.95
ATOM   2497  CB  ALA A 374      48.155   9.668  33.455  1.00 62.66
ATOM   2498  N   THR A 375      50.477  12.002  32.977  1.00 61.03
ATOM   2499  CA  THR A 375      51.919  12.320  32.715  1.00 60.30
ATOM   2500  C   THR A 375      52.401  12.358  31.269  1.00 58.41
ATOM   2501  O   THR A 375      52.361  11.308  30.555  1.00 59.21
ATOM   2502  CB  THR A 375      52.838  11.327  33.455  1.00 61.35
ATOM   2503  OG1 THR A 375      52.302  11.049  34.756  1.00 62.26
ATOM   2504  CG2 THR A 375      54.237  11.912  33.599  1.00 61.47
ATOM   2505  N   SER A 376      52.892  13.520  30.833  1.00 55.18
ATOM   2506  CA  SER A 376      53.407  13.683  29.445  1.00 51.40
ATOM   2507  C   SER A 376      53.538  15.132  28.981  1.00 48.79
ATOM   2508  O   SER A 376      52.887  16.067  29.540  1.00 48.19
ATOM   2509  CB  SER A 376      52.502  12.943  28.456  1.00 51.90
ATOM   2510  OG  SER A 376      52.880  13.193  27.115  1.00 51.94
ATOM   2511  N   GLN A 377      54.373  15.333  27.968  1.00 44.88
ATOM   2512  CA  GLN A 377      54.576  16.664  27.367  1.00 41.28
ATOM   2513  C   GLN A 377      54.106  16.580  25.923  1.00 37.22
ATOM   2514  O   GLN A 377      54.380  17.489  25.081  1.00 35.23
ATOM   2515  CB  GLN A 377      56.048  17.062  27.425  1.00 43.59
ATOM   2516  CG  GLN A 377      56.468  17.585  28.789  1.00 46.22
ATOM   2517  CD  GLN A 377      57.955  17.831  28.886  1.00 47.12
ATOM   2518  OE1 GLN A 377      58.710  17.710  27.867  1.00 48.44
ATOM   2519  NE2 GLN A 377      58.414  18.177  30.081  1.00 48.23
ATOM   2520  N   ASP A 378      53.399  15.499  25.618  1.00 31.89
ATOM   2521  CA  ASP A 378      52.866  15.289  24.263  1.00 28.31
ATOM   2522  C   ASP A 378      51.663  16.183  24.034  1.00 25.36
ATOM   2523  O   ASP A 378      50.958  16.590  25.004  1.00 22.58
ATOM   2524  CB  ASP A 378      52.422  13.835  24.072  1.00 28.64
ATOM   2525  CG  ASP A 378      53.582  12.867  23.998  1.00 29.19
ATOM   2526  OD1 ASP A 378      54.746  13.316  23.948  1.00 30.91
ATOM   2527  OD2 ASP A 378      53.323  11.647  23.981  1.00 30.50
ATOM   2528  N   ASP A 379      51.415  16.513  22.776  1.00 23.06
ATOM   2529  CA  ASP A 379      50.236  17.317  22.436  1.00 22.51
ATOM   2530  C   ASP A 379      49.220  16.294  21.964  1.00 21.46
ATOM   2531  O   ASP A 379      49.436  15.581  20.945  1.00 19.87
ATOM   2532  CB  ASP A 379      50.570  18.335  21.346  1.00 21.72
ATOM   2533  CG  ASP A 379      51.557  19.377  21.829  1.00 23.29
ATOM   2534  OD1 ASP A 379      51.434  19.786  23.005  1.00 23.00
ATOM   2535  OD2 ASP A 379      52.446  19.789  21.052  1.00 23.50
ATOM   2536  N   CYS A 380      48.128  16.182  22.706  1.00 20.99
ATOM   2537  CA  CYS A 380      47.082  15.201  22.393  1.00 20.40
ATOM   2538  C   CYS A 380      45.769  15.865  22.013  1.00 19.94
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ATOM	2539	O	CYS	A	380	45.489	17.038	22.417	1.00 18.77
ATOM	2540	CB	CYS	A	380	46.867	14.292	23.596	1.00 23.14
ATOM	2541	SG	CYS	A	380	48.368	13.550	24.327	1.00 25.25
ATOM	2542	N	TYR	A	381	44.947	15.140	21.255	1.00 18.49
ATOM	2543	CA	TYR	A	381	43.656	15.681	20.785	1.00 17.31
ATOM	2544	C	TYR	A	381	42.595	14.610	20.602	1.00 17.45
ATOM	2545	O	TYR	A	381	42.890	13.376	20.532	1.00 16.46
ATOM	2546	CB	TYR	A	381	43.833	16.370	19.427	1.00 15.47
ATOM	2547	CG	TYR	A	381	45.034	17.275	19.314	1.00 14.93
ATOM	2548	CD1	TYR	A	381	44.899	18.659	19.408	1.00 14.20
ATOM	2549	CD2	TYR	A	381	46.311	16.746	19.118	1.00 14.17
ATOM	2550	CE1	TYR	A	381	46.009	19.499	19.307	1.00 14.66
ATOM	2551	CE2	TYR	A	381	47.431	17.576	19.021	1.00 15.73
ATOM	2552	CZ	TYR	A	381	47.272	18.952	19.113	1.00 16.02
ATOM	2553	OH	TYR	A	381	48.369	19.785	18.994	1.00 15.32
ATOM	2554	N	LYS	A	382	41.356	15.066	20.506	1.00 18.35
ATOM	2555	CA	LYS	A	382	40.218	14.174	20.248	1.00 20.26
ATOM	2556	C	LYS	A	382	39.555	14.695	18.981	1.00 19.31
ATOM	2557	O	LYS	A	382	39.575	15.941	18.704	1.00 19.65
ATOM	2558	CB	LYS	A	382	39.221	14.204	21.404	1.00 21.74
ATOM	2559	CG	LYS	A	382	39.632	13.348	22.585	1.00 25.42
ATOM	2560	CD	LYS	A	382	38.509	13.266	23.602	1.00 27.59
ATOM	2561	CE	LYS	A	382	38.878	12.342	24.759	1.00 29.84
ATOM	2562	NZ	LYS	A	382	37.779	12.246	25.761	1.00 31.22
ATOM	2563	N	PHE	A	383	38.994	13.786	18.192	1.00 18.55
ATOM	2564	CA	PHE	A	383	38.298	14.165	16.942	1.00 16.97
ATOM	2565	C	PHE	A	383	36.992	14.823	17.375	1.00 16.22
ATOM	2566	O	PHE	A	383	36.079	14.138	17.908	1.00 13.73
ATOM	2567	CB	PHE	A	383	38.026	12.907	16.110	1.00 16.57
ATOM	2568	CG	PHE	A	383	37.447	13.182	14.750	1.00 16.49
ATOM	2569	CD1	PHE	A	383	38.052	14.091	13.890	1.00 14.48
ATOM	2570	CD2	PHE	A	383	36.319	12.489	14.308	1.00 15.06
ATOM	2571	CE1	PHE	A	383	37.542	14.306	12.606	1.00 16.02
ATOM	2572	CE2	PHE	A	383	35.807	12.696	13.029	1.00 15.64
ATOM	2573	CZ	PHE	A	383	36.419	13.603	12.176	1.00 15.10
ATOM	2574	N	ALA	A	384	36.885	16.134	17.173	1.00 16.28
ATOM	2575	CA	ALA	A	384	35.675	16.893	17.586	1.00 15.54
ATOM	2576	C	ALA	A	384	34.549	16.931	16.559	1.00 15.46
ATOM	2577	O	ALA	A	384	33.768	17.931	16.487	1.00 15.60
ATOM	2578	CB	ALA	A	384	36.061	18.316	17.987	1.00 14.96
ATOM	2579	N	ILE	A	385	34.451	15.888	15.745	1.00 14.66
ATOM	2580	CA	ILE	A	385	33.356	15.792	14.763	1.00 13.45
ATOM	2581	C	ILE	A	385	32.651	14.487	15.093	1.00 14.39
ATOM	2582	O	ILE	A	385	33.303	13.410	15.179	1.00 12.37
ATOM	2583	CB	ILE	A	385	33.862	15.724	13.315	1.00 12.54
ATOM	2584	CG1	ILE	A	385	34.696	16.959	12.988	1.00 13.08
ATOM	2585	CG2	ILE	A	385	32.675	15.655	12.367	1.00 12.56
ATOM	2586	CD1	ILE	A	385	35.178	17.003	11.549	1.00 10.74
ATOM	2587	N	SER	A	386	31.343	14.543	15.297	1.00 14.95
ATOM	2588	CA	SER	A	386	30.605	13.319	15.637	1.00 16.99
ATOM	2589	C	SER	A	386	29.275	13.221	14.918	1.00 17.48
ATOM	2590	O	SER	A	386	28.795	14.207	14.279	1.00 18.09
ATOM	2591	CB	SER	A	386	30.385	13.240	17.151	1.00 16.69
ATOM	2592	OG	SER	A	386	29.630	14.345	17.616	1.00 16.81
ATOM	2593	N	GLN	A	387	28.673	12.044	15.016	1.00 19.86
ATOM	2594	CA	GLN	A	387	27.384	11.748	14.376	1.00 23.09
ATOM	2595	C	GLN	A	387	26.209	12.317	15.160	1.00 22.61
ATOM	2596	O	GLN	A	387	26.221	12.363	16.427	1.00 22.90
ATOM	2597	CB	GLN	A	387	27.222	10.234	14.247	1.00 24.53
ATOM	2598	CG	GLN	A	387	26.035	9.795	13.411	1.00 28.94
ATOM	2599	CD	GLN	A	387	25.971	8.286	13.272	1.00 30.39
ATOM	2600	OE1	GLN	A	387	27.013	7.619	12.999	1.00 31.54

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ATOM   2601  NE2 GLN A 387      24.782   7.721  13.441  1.00 32.07
ATOM   2602  N   SER A 388      25.186  12.743  14.434  1.00 21.60
ATOM   2603  CA  SER A 388      23.981  13.306  15.055  1.00 21.59
ATOM   2604  C   SER A 388      22.728  12.711  14.429  1.00 22.68
ATOM   2605  O   SER A 388      22.707  12.380  13.203  1.00 23.08
ATOM   2606  CB  SER A 388      23.959  14.824  14.871  1.00 19.88
ATOM   2607  OG  SER A 388      22.661  15.342  15.112  1.00 19.18
ATOM   2608  N   SER A 389      21.681  12.551  15.227  1.00 23.51
ATOM   2609  CA  SER A 389      20.405  12.024  14.690  1.00 24.44
ATOM   2610  C   SER A 389      19.391  13.167  14.708  1.00 23.83
ATOM   2611  O   SER A 389      18.181  12.973  14.385  1.00 23.81
ATOM   2612  CB  SER A 389      19.902  10.847  15.534  1.00 25.63
ATOM   2613  OG  SER A 389      19.681  11.235  16.881  1.00 27.65
ATOM   2614  N   THR A 390      19.861  14.360  15.066  1.00 22.66
ATOM   2615  CA  THR A 390      18.984  15.553  15.127  1.00 22.60
ATOM   2616  C   THR A 390      19.471  16.709  14.260  1.00 21.12
ATOM   2617  O   THR A 390      19.272  17.910  14.608  1.00 21.35
ATOM   2618  CB  THR A 390      18.825  16.052  16.577  1.00 23.02
ATOM   2619  OG1 THR A 390      20.117  16.288  17.150  1.00 24.55
ATOM   2620  CG2 THR A 390      18.079  15.010  17.413  1.00 23.83
ATOM   2621  N   GLY A 391      20.093  16.381  13.136  1.00 19.75
ATOM   2622  CA  GLY A 391      20.573  17.410  12.237  1.00 16.88
ATOM   2623  C   GLY A 391      21.982  17.891  12.526  1.00 17.24
ATOM   2624  O   GLY A 391      22.672  17.402  13.472  1.00 16.27
ATOM   2625  N   THR A 392      22.427  18.851  11.730  1.00 14.99
ATOM   2626  CA  THR A 392      23.773  19.423  11.880  1.00 14.81
ATOM   2627  C   THR A 392      23.841  20.514  12.938  1.00 14.47
ATOM   2628  O   THR A 392      22.949  21.409  13.012  1.00 16.11
ATOM   2629  CB  THR A 392      24.266  20.062  10.564  1.00 12.95
ATOM   2630  OG1 THR A 392      24.494  19.043   9.588  1.00 14.51
ATOM   2631  CG2 THR A 392      25.572  20.839  10.800  1.00 14.09
ATOM   2632  N   VAL A 393      24.857  20.458  13.779  1.00 13.06
ATOM   2633  CA  VAL A 393      25.027  21.534  14.746  1.00 15.07
ATOM   2634  C   VAL A 393      26.462  22.033  14.684  1.00 15.47
ATOM   2635  O   VAL A 393      27.450  21.265  14.908  1.00 16.85
ATOM   2636  CB  VAL A 393      24.619  21.128  16.201  1.00 16.35
ATOM   2637  CG1 VAL A 393      24.559  19.624  16.348  1.00 15.06
ATOM   2638  CG2 VAL A 393      25.566  21.766  17.210  1.00 13.79
ATOM   2639  N   MET A 394      26.592  23.298  14.312  1.00 15.41
ATOM   2640  CA  MET A 394      27.900  23.962  14.231  1.00 16.55
ATOM   2641  C   MET A 394      28.188  24.442  15.647  1.00 16.43
ATOM   2642  O   MET A 394      27.737  25.553  16.059  1.00 14.99
ATOM   2643  CB  MET A 394      27.822  25.143  13.264  1.00 16.88
ATOM   2644  CG  MET A 394      27.607  24.724  11.818  1.00 21.12
ATOM   2645  SD  MET A 394      27.178  26.083  10.700  1.00 27.34
ATOM   2646  CE  MET A 394      25.475  25.768  10.522  1.00 26.22
ATOM   2647  N   GLY A 395      28.909  23.622  16.406  1.00 16.28
ATOM   2648  CA  GLY A 395      29.220  23.967  17.780  1.00 15.87
ATOM   2649  C   GLY A 395      30.487  24.775  17.971  1.00 16.72
ATOM   2650  O   GLY A 395      31.011  25.408  17.005  1.00 16.25
ATOM   2651  N   ALA A 396      30.989  24.769  19.202  1.00 17.29
ATOM   2652  CA  ALA A 396      32.211  25.511  19.586  1.00 19.21
ATOM   2653  C   ALA A 396      33.383  25.310  18.634  1.00 19.63
ATOM   2654  O   ALA A 396      34.050  26.303  18.223  1.00 22.56
ATOM   2655  CB  ALA A 396      32.626  25.128  21.013  1.00 16.95
ATOM   2656  N   VAL A 397      33.661  24.065  18.269  1.00 21.31
ATOM   2657  CA  VAL A 397      34.792  23.781  17.353  1.00 23.40
ATOM   2658  C   VAL A 397      34.690  24.592  16.068  1.00 21.89
ATOM   2659  O   VAL A 397      35.731  25.029  15.496  1.00 24.15
ATOM   2660  CB  VAL A 397      34.874  22.274  17.012  1.00 24.19
ATOM   2661  CG1 VAL A 397      35.065  21.480  18.287  1.00 26.91
ATOM   2662  CG2 VAL A 397      33.623  21.826  16.290  1.00 25.89
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ATOM	2663	N	ILE	A	398	33.472	24.805	15.586	1.00 21.78
ATOM	2664	CA	ILE	A	398	33.276	25.612	14.359	1.00 21.50
ATOM	2665	C	ILE	A	398	33.403	27.086	14.735	1.00 19.91
ATOM	2666	O	ILE	A	398	34.222	27.849	14.135	1.00 16.77
ATOM	2667	CB	ILE	A	398	31.872	25.390	13.749	1.00 23.48
ATOM	2668	CG1	ILE	A	398	31.859	24.113	12.910	1.00 26.70
ATOM	2669	CG2	ILE	A	398	31.469	26.596	12.895	1.00 24.67
ATOM	2670	CD1	ILE	A	398	32.656	24.223	11.620	1.00 27.64
ATOM	2671	N	MET	A	399	32.614	27.492	15.726	1.00 17.64
ATOM	2672	CA	MET	A	399	32.594	28.889	16.201	1.00 16.99
ATOM	2673	C	MET	A	399	33.951	29.439	16.640	1.00 17.65
ATOM	2674	O	MET	A	399	34.202	30.677	16.517	1.00 18.70
ATOM	2675	CB	MET	A	399	31.575	29.025	17.331	1.00 15.33
ATOM	2676	CG	MET	A	399	30.138	28.800	16.866	1.00 14.30
ATOM	2677	SD	MET	A	399	28.891	29.038	18.155	1.00 16.41
ATOM	2678	CE	MET	A	399	28.972	30.826	18.388	1.00 10.15
ATOM	2679	N	GLU	A	400	34.835	28.579	17.143	1.00 16.09
ATOM	2680	CA	GLU	A	400	36.175	29.051	17.580	1.00 16.46
ATOM	2681	C	GLU	A	400	36.968	29.576	16.389	1.00 14.50
ATOM	2682	O	GLU	A	400	37.971	30.332	16.553	1.00 14.83
ATOM	2683	CB	GLU	A	400	36.957	27.919	18.257	1.00 15.95
ATOM	2684	CG	GLU	A	400	36.318	27.419	19.540	1.00 18.44
ATOM	2685	CD	GLU	A	400	37.156	26.376	20.243	1.00 18.72
ATOM	2686	OE1	GLU	A	400	37.771	25.542	19.546	1.00 20.29
ATOM	2687	OE2	GLU	A	400	37.186	26.383	21.493	1.00 19.60
ATOM	2688	N	GLY	A	401	36.544	29.204	15.190	1.00 13.62
ATOM	2689	CA	GLY	A	401	37.246	29.662	14.010	1.00 15.09
ATOM	2690	C	GLY	A	401	36.747	31.010	13.533	1.00 16.28
ATOM	2691	O	GLY	A	401	37.435	31.693	12.716	1.00 16.14
ATOM	2692	N	PHE	A	402	35.591	31.438	14.033	1.00 14.90
ATOM	2693	CA	PHE	A	402	35.018	32.712	13.572	1.00 15.01
ATOM	2694	C	PHE	A	402	34.378	33.605	14.615	1.00 15.52
ATOM	2695	O	PHE	A	402	34.078	33.185	15.777	1.00 16.47
ATOM	2696	CB	PHE	A	402	33.966	32.424	12.495	1.00 14.48
ATOM	2697	CG	PHE	A	402	34.381	31.364	11.522	1.00 15.64
ATOM	2698	CD1	PHE	A	402	34.126	30.021	11.785	1.00 14.91
ATOM	2699	CD2	PHE	A	402	35.095	31.700	10.376	1.00 15.20
ATOM	2700	CE1	PHE	A	402	34.581	29.027	10.920	1.00 15.18
ATOM	2701	CE2	PHE	A	402	35.555	30.717	9.507	1.00 15.72
ATOM	2702	CZ	PHE	A	402	35.298	29.376	9.782	1.00 15.12
ATOM	2703	N	TYR	A	403	34.168	34.847	14.208	1.00 15.73
ATOM	2704	CA	TYR	A	403	33.474	35.837	15.039	1.00 15.81
ATOM	2705	C	TYR	A	403	32.071	35.641	14.489	1.00 14.48
ATOM	2706	O	TYR	A	403	31.846	35.789	13.250	1.00 15.47
ATOM	2707	CB	TYR	A	403	33.977	37.251	14.731	1.00 14.45
ATOM	2708	CG	TYR	A	403	33.265	38.340	15.499	1.00 15.22
ATOM	2709	CD1	TYR	A	403	32.899	38.152	16.834	1.00 14.85
ATOM	2710	CD2	TYR	A	403	33.018	39.584	14.916	1.00 14.28
ATOM	2711	CE1	TYR	A	403	32.311	39.175	17.569	1.00 15.25
ATOM	2712	CE2	TYR	A	403	32.435	40.617	15.644	1.00 14.12
ATOM	2713	CZ	TYR	A	403	32.086	40.406	16.967	1.00 15.72
ATOM	2714	OH	TYR	A	403	31.525	41.427	17.697	1.00 18.09
ATOM	2715	N	VAL	A	404	31.125	35.286	15.345	1.00 14.70
ATOM	2716	CA	VAL	A	404	29.753	35.040	14.854	1.00 14.44
ATOM	2717	C	VAL	A	404	28.759	36.079	15.342	1.00 14.92
ATOM	2718	O	VAL	A	404	28.552	36.259	16.582	1.00 15.62
ATOM	2719	CB	VAL	A	404	29.284	33.629	15.260	1.00 14.39
ATOM	2720	CG1	VAL	A	404	27.925	33.323	14.640	1.00 11.90
ATOM	2721	CG2	VAL	A	404	30.327	32.603	14.819	1.00 12.73
ATOM	2722	N	VAL	A	405	28.136	36.762	14.386	1.00 16.06
ATOM	2723	CA	VAL	A	405	27.153	37.822	14.676	1.00 14.31
ATOM	2724	C	VAL	A	405	25.717	37.312	14.562	1.00 16.79

ATOM	2725	O	VAL	A	405	25.238	36.955	13.443	1.00	16.14
ATOM	2726	CB	VAL	A	405	27.318	39.004	13.700	1.00	13.66
ATOM	2727	CG1	VAL	A	405	26.302	40.092	14.021	1.00	12.39
ATOM	2728	CG2	VAL	A	405	28.739	39.547	13.775	1.00	10.80
ATOM	2729	N	PHE	A	406	25.019	37.260	15.691	1.00	16.73
ATOM	2730	CA	PHE	A	406	23.616	36.805	15.685	1.00	16.71
ATOM	2731	C	PHE	A	406	22.755	38.049	15.531	1.00	17.47
ATOM	2732	O	PHE	A	406	22.286	38.654	16.539	1.00	17.39
ATOM	2733	CB	PHE	A	406	23.287	36.053	16.979	1.00	13.96
ATOM	2734	CG	PHE	A	406	24.061	34.765	17.139	1.00	13.82
ATOM	2735	CD1	PHE	A	406	25.398	34.783	17.533	1.00	13.31
ATOM	2736	CD2	PHE	A	406	23.464	33.538	16.863	1.00	12.85
ATOM	2737	CE1	PHE	A	406	26.128	33.601	17.646	1.00	13.23
ATOM	2738	CE2	PHE	A	406	24.185	32.350	16.973	1.00	12.78
ATOM	2739	CZ	PHE	A	406	25.522	32.382	17.367	1.00	12.96
ATOM	2740	N	ASP	A	407	22.566	38.449	14.278	1.00	18.08
ATOM	2741	CA	ASP	A	407	21.785	39.647	13.932	1.00	19.70
ATOM	2742	C	ASP	A	407	20.297	39.316	13.927	1.00	19.73
ATOM	2743	O	ASP	A	407	19.675	39.120	12.837	1.00	18.96
ATOM	2744	CB	ASP	A	407	22.221	40.153	12.552	1.00	22.61
ATOM	2745	CG	ASP	A	407	21.663	41.530	12.223	1.00	24.28
ATOM	2746	OD1	ASP	A	407	20.660	41.935	12.849	1.00	24.12
ATOM	2747	OD2	ASP	A	407	22.225	42.198	11.325	1.00	23.37
ATOM	2748	N	ARG	A	408	19.709	39.245	15.116	1.00	19.72
ATOM	2749	CA	ARG	A	408	18.269	38.928	15.259	1.00	22.01
ATOM	2750	C	ARG	A	408	17.393	39.967	14.557	1.00	21.56
ATOM	2751	O	ARG	A	408	16.386	39.606	13.875	1.00	20.49
ATOM	2752	CB	ARG	A	408	17.909	38.835	16.748	1.00	23.44
ATOM	2753	CG	ARG	A	408	18.670	37.724	17.479	1.00	25.61
ATOM	2754	CD	ARG	A	408	18.838	37.994	18.973	1.00	28.14
ATOM	2755	NE	ARG	A	408	17.843	37.328	19.814	1.00	31.17
ATOM	2756	CZ	ARG	A	408	16.567	37.679	19.887	1.00	32.24
ATOM	2757	NH1	ARG	A	408	16.127	38.693	19.163	1.00	35.70
ATOM	2758	NH2	ARG	A	408	15.735	37.029	20.687	1.00	31.13
ATOM	2759	N	ALA	A	409	17.750	41.241	14.694	1.00	21.10
ATOM	2760	CA	ALA	A	409	16.978	42.329	14.056	1.00	22.43
ATOM	2761	C	ALA	A	409	16.785	42.050	12.571	1.00	22.80
ATOM	2762	O	ALA	A	409	15.646	42.177	12.034	1.00	24.04
ATOM	2763	CB	ALA	A	409	17.689	43.664	14.247	1.00	20.85
ATOM	2764	N	ARG	A	410	17.858	41.664	11.889	1.00	23.89
ATOM	2765	CA	ARG	A	410	17.770	41.374	10.445	1.00	25.07
ATOM	2766	C	ARG	A	410	17.639	39.888	10.119	1.00	24.26
ATOM	2767	O	ARG	A	410	17.908	39.461	8.956	1.00	24.63
ATOM	2768	CB	ARG	A	410	18.987	41.949	9.724	1.00	26.83
ATOM	2769	CG	ARG	A	410	19.025	43.464	9.700	1.00	29.89
ATOM	2770	CD	ARG	A	410	19.326	43.944	8.295	1.00	32.69
ATOM	2771	NE	ARG	A	410	20.590	44.664	8.208	1.00	33.51
ATOM	2772	CZ	ARG	A	410	21.182	44.979	7.062	1.00	34.58
ATOM	2773	NH1	ARG	A	410	20.626	44.631	5.907	1.00	33.99
ATOM	2774	NH2	ARG	A	410	22.328	45.644	7.068	1.00	35.27
ATOM	2775	N	LYS	A	411	17.223	39.091	11.097	1.00	22.77
ATOM	2776	CA	LYS	A	411	17.061	37.630	10.891	1.00	22.97
ATOM	2777	C	LYS	A	411	18.227	37.031	10.104	1.00	21.80
ATOM	2778	O	LYS	A	411	18.015	36.309	9.081	1.00	20.39
ATOM	2779	CB	LYS	A	411	15.761	37.335	10.138	1.00	23.53
ATOM	2780	CG	LYS	A	411	14.491	37.686	10.886	1.00	27.80
ATOM	2781	CD	LYS	A	411	13.270	37.188	10.121	1.00	30.25
ATOM	2782	CE	LYS	A	411	13.337	35.678	9.890	1.00	31.18
ATOM	2783	NZ	LYS	A	411	12.153	35.163	9.142	1.00	34.08
ATOM	2784	N	ARG	A	412	19.449	37.290	10.541	1.00	19.85
ATOM	2785	CA	ARG	A	412	20.607	36.748	9.815	1.00	18.29
ATOM	2786	C	ARG	A	412	21.789	36.505	10.736	1.00	18.54

ATOM	2787	O	ARG	A	412	21.911	37.137	11.837	1.00 18.56
ATOM	2788	CB	ARG	A	412	21.019	37.714	8.703	1.00 18.72
ATOM	2789	CG	ARG	A	412	21.571	39.027	9.239	1.00 18.66
ATOM	2790	CD	ARG	A	412	21.941	39.988	8.127	1.00 18.34
ATOM	2791	NE	ARG	A	412	22.560	41.196	8.662	1.00 19.28
ATOM	2792	CZ	ARG	A	412	23.082	42.163	7.916	1.00 20.03
ATOM	2793	NH1	ARG	A	412	23.059	42.067	6.591	1.00 19.36
ATOM	2794	NH2	ARG	A	412	23.635	43.219	8.496	1.00 19.27
ATOM	2795	N	ILE	A	413	22.668	35.606	10.317	1.00 17.01
ATOM	2796	CA	ILE	A	413	23.865	35.285	11.103	1.00 16.43
ATOM	2797	C	ILE	A	413	25.103	35.576	10.266	1.00 16.20
ATOM	2798	O	ILE	A	413	25.213	35.125	9.084	1.00 17.17
ATOM	2799	CB	ILE	A	413	23.855	33.808	11.533	1.00 16.02
ATOM	2800	CG1	ILE	A	413	22.667	33.562	12.469	1.00 13.92
ATOM	2801	CG2	ILE	A	413	25.168	33.458	12.218	1.00 15.95
ATOM	2802	CD1	ILE	A	413	22.482	32.130	12.862	1.00 14.89
ATOM	2803	N	GLY	A	414	26.028	36.332	10.841	1.00 15.43
ATOM	2804	CA	GLY	A	414	27.243	36.679	10.132	1.00 14.42
ATOM	2805	C	GLY	A	414	28.463	35.899	10.585	1.00 14.91
ATOM	2806	O	GLY	A	414	28.569	35.463	11.779	1.00 12.74
ATOM	2807	N	PHE	A	415	29.392	35.709	9.656	1.00 12.70
ATOM	2808	CA	PHE	A	415	30.638	34.977	9.932	1.00 14.84
ATOM	2809	C	PHE	A	415	31.823	35.766	9.403	1.00 15.05
ATOM	2810	O	PHE	A	415	31.761	36.376	8.291	1.00 17.34
ATOM	2811	CB	PHE	A	415	30.613	33.599	9.256	1.00 13.57
ATOM	2812	CG	PHE	A	415	29.628	32.640	9.860	1.00 13.35
ATOM	2813	CD1	PHE	A	415	30.034	31.710	10.820	1.00 14.56
ATOM	2814	CD2	PHE	A	415	28.296	32.660	9.472	1.00 11.54
ATOM	2815	CE1	PHE	A	415	29.117	30.809	11.383	1.00 13.74
ATOM	2816	CE2	PHE	A	415	27.373	31.768	10.027	1.00 12.67
ATOM	2817	CZ	PHE	A	415	27.787	30.839	10.985	1.00 13.15
ATOM	2818	N	ALA	A	416	32.895	35.779	10.178	1.00 15.11
ATOM	2819	CA	ALA	A	416	34.135	36.470	9.786	1.00 14.57
ATOM	2820	C	ALA	A	416	35.248	35.738	10.515	1.00 14.48
ATOM	2821	O	ALA	A	416	35.027	35.186	11.639	1.00 12.56
ATOM	2822	CB	ALA	A	416	34.095	37.935	10.208	1.00 11.46
ATOM	2823	N	VAL	A	417	36.425	35.692	9.906	1.00 14.71
ATOM	2824	CA	VAL	A	417	37.569	35.011	10.528	1.00 16.80
ATOM	2825	C	VAL	A	417	37.835	35.634	11.892	1.00 18.08
ATOM	2826	O	VAL	A	417	37.922	36.901	12.033	1.00 17.13
ATOM	2827	CB	VAL	A	417	38.824	35.126	9.642	1.00 17.67
ATOM	2828	CG1	VAL	A	417	40.022	34.486	10.333	1.00 16.83
ATOM	2829	CG2	VAL	A	417	38.561	34.441	8.301	1.00 18.32
ATOM	2830	N	SER	A	418	37.953	34.785	12.905	1.00 17.31
ATOM	2831	CA	SER	A	418	38.201	35.271	14.272	1.00 17.62
ATOM	2832	C	SER	A	418	39.637	35.712	14.455	1.00 18.36
ATOM	2833	O	SER	A	418	40.591	35.038	13.963	1.00 19.44
ATOM	2834	CB	SER	A	418	37.882	34.182	15.295	1.00 18.09
ATOM	2835	OG	SER	A	418	38.228	34.617	16.599	1.00 17.42
ATOM	2836	N	ALA	A	419	39.821	36.827	15.150	1.00 17.60
ATOM	2837	CA	ALA	A	419	41.175	37.335	15.410	1.00 18.46
ATOM	2838	C	ALA	A	419	41.877	36.423	16.423	1.00 19.09
ATOM	2839	O	ALA	A	419	43.117	36.553	16.649	1.00 19.60
ATOM	2840	CB	ALA	A	419	41.106	38.772	15.943	1.00 17.70
ATOM	2841	N	CYS	A	420	41.132	35.500	17.032	1.00 19.36
ATOM	2842	CA	CYS	A	420	41.736	34.575	18.029	1.00 20.89
ATOM	2843	C	CYS	A	420	41.677	33.105	17.624	1.00 19.60
ATOM	2844	O	CYS	A	420	41.805	32.202	18.501	1.00 22.74
ATOM	2845	CB	CYS	A	420	41.064	34.734	19.410	1.00 21.69
ATOM	2846	SG	CYS	A	420	39.353	34.096	19.526	1.00 25.02
ATOM	2847	N	HIS	A	421	41.495	32.814	16.342	1.00 17.86
ATOM	2848	CA	HIS	A	421	41.435	31.393	15.933	1.00 17.71

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ATOM   2849  C   HIS A 421      42.834  30.798  15.799  1.00 17.18
ATOM   2850  O   HIS A 421      43.801  31.495  15.356  1.00 14.17
ATOM   2851  CB  HIS A 421      40.641  31.236  14.625  1.00 18.65
ATOM   2852  CG  HIS A 421      41.433  31.504  13.381  1.00 18.77
ATOM   2853  ND1 HIS A 421      42.114  30.514  12.705  1.00 18.84
ATOM   2854  CD2 HIS A 421      41.631  32.645  12.678  1.00 18.73
ATOM   2855  CE1 HIS A 421      42.695  31.032  11.637  1.00 17.98
ATOM   2856  NE2 HIS A 421      42.418  32.323  11.597  1.00 20.03
ATOM   2857  N   VAL A 422      42.965  29.533  16.194  1.00 16.96
ATOM   2858  CA  VAL A 422      44.260  28.816  16.132  1.00 16.89
ATOM   2859  C   VAL A 422      44.571  28.334  14.719  1.00 17.53
ATOM   2860  O   VAL A 422      43.678  27.764  14.021  1.00 17.13
ATOM   2861  CB  VAL A 422      44.257  27.588  17.061  1.00 16.92
ATOM   2862  CG1 VAL A 422      45.632  26.938  17.063  1.00 15.15
ATOM   2863  CG2 VAL A 422      43.850  28.004  18.479  1.00 19.33
ATOM   2864  N   HIS A 423      45.815  28.531  14.291  1.00 16.64
ATOM   2865  CA  HIS A 423      46.264  28.112  12.940  1.00 16.92
ATOM   2866  C   HIS A 423      47.792  28.038  12.906  1.00 17.46
ATOM   2867  O   HIS A 423      48.461  28.105  13.981  1.00 17.20
ATOM   2868  CB  HIS A 423      45.755  29.111  11.889  1.00 15.85
ATOM   2869  CG  HIS A 423      46.242  30.512  12.096  1.00 18.62
ATOM   2870  ND1 HIS A 423      47.390  30.998  11.504  1.00 19.80
ATOM   2871  CD2 HIS A 423      45.758  31.522  12.857  1.00 17.42
ATOM   2872  CE1 HIS A 423      47.590  32.245  11.892  1.00 18.22
ATOM   2873  NE2 HIS A 423      46.615  32.586  12.714  1.00 18.53
ATOM   2874  N   ASP A 424      48.360  27.869  11.714  1.00 18.00
ATOM   2875  CA  ASP A 424      49.836  27.817  11.556  1.00 17.75
ATOM   2876  C   ASP A 424      50.194  28.804  10.453  1.00 18.36
ATOM   2877  O   ASP A 424      49.294  29.527   9.935  1.00 20.02
ATOM   2878  CB  ASP A 424      50.305  26.396  11.206  1.00 18.00
ATOM   2879  CG  ASP A 424      49.545  25.791  10.037  1.00 19.08
ATOM   2880  OD1 ASP A 424      49.110  24.623  10.149  1.00 18.99
ATOM   2881  OD2 ASP A 424      49.390  26.473   9.003  1.00 20.46
ATOM   2882  N   GLU A 425      51.459  28.877  10.063  1.00 17.55
ATOM   2883  CA  GLU A 425      51.813  29.853   9.015  1.00 18.77
ATOM   2884  C   GLU A 425      51.497  29.379   7.601  1.00 16.95
ATOM   2885  O   GLU A 425      51.724  30.131   6.613  1.00 17.24
ATOM   2886  CB  GLU A 425      53.289  30.239   9.112  1.00 18.65
ATOM   2887  CG  GLU A 425      54.254  29.150   8.714  1.00 20.84
ATOM   2888  CD  GLU A 425      55.632  29.697   8.381  1.00 21.89
ATOM   2889  OE1 GLU A 425      56.481  28.901   7.936  1.00 22.61
ATOM   2890  OE2 GLU A 425      55.867  30.920   8.559  1.00 22.65
ATOM   2891  N   PHE A 426      50.955  28.171   7.476  1.00 14.60
ATOM   2892  CA  PHE A 426      50.619  27.606   6.150  1.00 13.51
ATOM   2893  C   PHE A 426      49.157  27.767   5.763  1.00 15.14
ATOM   2894  O   PHE A 426      48.826  27.822   4.540  1.00 16.10
ATOM   2895  CB  PHE A 426      51.001  26.127   6.109  1.00 14.53
ATOM   2896  CG  PHE A 426      52.452  25.877   6.400  1.00 14.20
ATOM   2897  CD1 PHE A 426      53.433  26.244   5.482  1.00 13.59
ATOM   2898  CD2 PHE A 426      52.841  25.298   7.606  1.00 14.11
ATOM   2899  CE1 PHE A 426      54.787  26.040   5.762  1.00 14.83
ATOM   2900  CE2 PHE A 426      54.192  25.087   7.897  1.00 15.49
ATOM   2901  CZ  PHE A 426      55.167  25.460   6.969  1.00 14.08
ATOM   2902  N   ARG A 427      48.269  27.827   6.752  1.00 13.77
ATOM   2903  CA  ARG A 427      46.824  27.985   6.469  1.00 14.89
ATOM   2904  C   ARG A 427      46.130  28.695   7.615  1.00 15.43
ATOM   2905  O   ARG A 427      46.630  28.710   8.781  1.00 14.58
ATOM   2906  CB  ARG A 427      46.132  26.632   6.301  1.00 15.33
ATOM   2907  CG  ARG A 427      46.959  25.518   5.707  1.00 16.84
ATOM   2908  CD  ARG A 427      46.645  24.234   6.477  1.00 17.68
ATOM   2909  NE  ARG A 427      45.994  23.230   5.655  1.00 16.69
ATOM   2910  CZ  ARG A 427      45.701  21.998   6.062  1.00 15.45
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ATOM	2911	NH1	ARG	A	427	45.114	21.159	5.224	1.00	14.20
ATOM	2912	NH2	ARG	A	427	45.981	21.603	7.296	1.00	13.31
ATOM	2913	N	THR	A	428	44.976	29.269	7.317	1.00	15.28
ATOM	2914	CA	THR	A	428	44.180	29.967	8.336	1.00	17.94
ATOM	2915	C	THR	A	428	42.731	29.650	8.041	1.00	16.25
ATOM	2916	O	THR	A	428	42.400	29.165	6.923	1.00	14.77
ATOM	2917	CB	THR	A	428	44.353	31.503	8.249	1.00	18.18
ATOM	2918	OG1	THR	A	428	44.043	31.942	6.921	1.00	20.24
ATOM	2919	CG2	THR	A	428	45.773	31.901	8.583	1.00	19.84
ATOM	2920	N	ALA	A	429	41.860	29.901	9.009	1.00	16.14
ATOM	2921	CA	ALA	A	429	40.423	29.677	8.803	1.00	16.03
ATOM	2922	C	ALA	A	429	40.048	30.739	7.775	1.00	15.66
ATOM	2923	O	ALA	A	429	40.808	31.738	7.574	1.00	14.51
ATOM	2924	CB	ALA	A	429	39.656	29.898	10.105	1.00	17.08
ATOM	2925	N	ALA	A	430	38.920	30.575	7.107	1.00	14.04
ATOM	2926	CA	ALA	A	430	38.556	31.576	6.100	1.00	13.71
ATOM	2927	C	ALA	A	430	37.067	31.706	5.883	1.00	11.98
ATOM	2928	O	ALA	A	430	36.271	30.754	6.166	1.00	12.33
ATOM	2929	CB	ALA	A	430	39.251	31.246	4.762	1.00	12.27
ATOM	2930	N	VAL	A	431	36.671	32.874	5.396	1.00	11.01
ATOM	2931	CA	VAL	A	431	35.260	33.149	5.076	1.00	13.39
ATOM	2932	C	VAL	A	431	35.344	33.773	3.697	1.00	15.69
ATOM	2933	O	VAL	A	431	35.857	34.926	3.533	1.00	17.86
ATOM	2934	CB	VAL	A	431	34.624	34.145	6.056	1.00	11.50
ATOM	2935	CG1	VAL	A	431	33.148	34.294	5.737	1.00	10.61
ATOM	2936	CG2	VAL	A	431	34.818	33.659	7.494	1.00	10.71
ATOM	2937	N	GLU	A	432	34.874	33.048	2.694	1.00	16.74
ATOM	2938	CA	GLU	A	432	34.969	33.544	1.320	1.00	18.65
ATOM	2939	C	GLU	A	432	33.681	33.414	0.530	1.00	18.40
ATOM	2940	O	GLU	A	432	32.794	32.567	0.852	1.00	16.81
ATOM	2941	CB	GLU	A	432	36.097	32.796	0.607	1.00	19.91
ATOM	2942	CG	GLU	A	432	37.460	33.031	1.241	1.00	24.66
ATOM	2943	CD	GLU	A	432	38.466	31.930	0.935	1.00	27.80
ATOM	2944	OE1	GLU	A	432	39.681	32.196	1.051	1.00	30.84
ATOM	2945	OE2	GLU	A	432	38.049	30.799	0.595	1.00	28.87
ATOM	2946	N	GLY	A	433	33.574	34.243	-0.504	1.00	18.95
ATOM	2947	CA	GLY	A	433	32.408	34.244	-1.363	1.00	19.36
ATOM	2948	C	GLY	A	433	32.504	35.385	-2.359	1.00	19.59
ATOM	2949	O	GLY	A	433	33.489	36.173	-2.328	1.00	18.33
ATOM	2950	N	PRO	A	434	31.511	35.539	-3.243	1.00	19.47
ATOM	2951	CA	PRO	A	434	30.345	34.655	-3.285	1.00	19.72
ATOM	2952	C	PRO	A	434	30.485	33.589	-4.353	1.00	19.98
ATOM	2953	O	PRO	A	434	31.382	33.674	-5.235	1.00	22.24
ATOM	2954	CB	PRO	A	434	29.215	35.619	-3.595	1.00	19.80
ATOM	2955	CG	PRO	A	434	29.869	36.517	-4.616	1.00	19.70
ATOM	2956	CD	PRO	A	434	31.261	36.770	-4.018	1.00	19.73
ATOM	2957	N	PHE	A	435	29.624	32.583	-4.290	1.00	21.45
ATOM	2958	CA	PHE	A	435	29.619	31.502	-5.292	1.00	22.31
ATOM	2959	C	PHE	A	435	28.217	31.513	-5.872	1.00	24.39
ATOM	2960	O	PHE	A	435	27.207	31.636	-5.110	1.00	24.58
ATOM	2961	CB	PHE	A	435	29.924	30.155	-4.636	1.00	22.02
ATOM	2962	CG	PHE	A	435	31.215	30.141	-3.876	1.00	20.80
ATOM	2963	CD1	PHE	A	435	31.232	30.392	-2.507	1.00	20.70
ATOM	2964	CD2	PHE	A	435	32.424	29.945	-4.542	1.00	21.70
ATOM	2965	CE1	PHE	A	435	32.432	30.451	-1.809	1.00	20.27
ATOM	2966	CE2	PHE	A	435	33.634	30.003	-3.853	1.00	21.68
ATOM	2967	CZ	PHE	A	435	33.637	30.259	-2.481	1.00	21.51
ATOM	2968	N	VAL	A	436	28.117	31.396	-7.192	1.00	27.02
ATOM	2969	CA	VAL	A	436	26.802	31.438	-7.872	1.00	29.79
ATOM	2970	C	VAL	A	436	26.526	30.219	-8.739	1.00	32.85
ATOM	2971	O	VAL	A	436	25.434	30.120	-9.376	1.00	33.81
ATOM	2972	CB	VAL	A	436	26.702	32.677	-8.787	1.00	28.98

ATOM	2973	CG1	VAL	A	436	26.999	33.944	-7.996	1.00	29.00
ATOM	2974	CG2	VAL	A	436	27.678	32.537	-9.947	1.00	28.49
ATOM	2975	N	THR	A	437	27.473	29.292	-8.795	1.00	36.05
ATOM	2976	CA	THR	A	437	27.305	28.089	-9.638	1.00	39.30
ATOM	2977	C	THR	A	437	26.582	26.979	-8.870	1.00	41.99
ATOM	2978	O	THR	A	437	26.604	25.775	-9.276	1.00	41.77
ATOM	2979	CB	THR	A	437	28.690	27.592	-10.123	1.00	39.02
ATOM	2980	OG1	THR	A	437	28.552	26.981	-11.408	1.00	42.51
ATOM	2981	CG2	THR	A	437	29.280	26.578	-9.156	1.00	38.10
ATOM	2982	N	LEU	A	438	25.908	27.368	-7.794	1.00	45.33
ATOM	2983	CA	LEU	A	438	25.199	26.417	-6.901	1.00	49.22
ATOM	2984	C	LEU	A	438	23.753	26.016	-7.165	1.00	50.49
ATOM	2985	O	LEU	A	438	22.869	26.878	-7.466	1.00	51.99
ATOM	2986	CB	LEU	A	438	25.276	26.944	-5.473	1.00	50.30
ATOM	2987	CG	LEU	A	438	26.027	28.269	-5.358	1.00	50.73
ATOM	2988	CD1	LEU	A	438	25.108	29.457	-5.584	1.00	50.27
ATOM	2989	CD2	LEU	A	438	26.629	28.328	-4.001	1.00	51.67
ATOM	2990	N	ASP	A	439	23.505	24.715	-7.037	1.00	52.67
ATOM	2991	CA	ASP	A	439	22.149	24.128	-7.172	1.00	55.74
ATOM	2992	C	ASP	A	439	21.690	24.224	-5.722	1.00	56.96
ATOM	2993	O	ASP	A	439	21.757	23.221	-4.945	1.00	57.33
ATOM	2994	CB	ASP	A	439	22.240	22.657	-7.586	1.00	56.39
ATOM	2995	CG	ASP	A	439	20.879	21.993	-7.695	1.00	57.68
ATOM	2996	OD1	ASP	A	439	20.046	22.178	-6.781	1.00	57.75
ATOM	2997	OD2	ASP	A	439	20.645	21.274	-8.692	1.00	58.18
ATOM	2998	N	MET	A	440	21.233	25.407	-5.337	1.00	58.71
ATOM	2999	CA	MET	A	440	20.841	25.656	-3.944	1.00	60.87
ATOM	3000	C	MET	A	440	19.435	26.215	-3.713	1.00	62.52
ATOM	3001	O	MET	A	440	19.247	27.451	-3.489	1.00	63.93
ATOM	3002	CB	MET	A	440	21.916	26.569	-3.346	1.00	60.48
ATOM	3003	CG	MET	A	440	21.523	27.456	-2.201	1.00	60.72
ATOM	3004	SD	MET	A	440	22.755	28.755	-2.086	1.00	59.28
ATOM	3005	CE	MET	A	440	22.367	29.689	-3.543	1.00	59.46
ATOM	3006	N	GLU	A	441	18.435	25.343	-3.765	1.00	63.61
ATOM	3007	CA	GLU	A	441	17.042	25.774	-3.514	1.00	65.54
ATOM	3008	C	GLU	A	441	16.356	24.847	-2.518	1.00	64.49
ATOM	3009	O	GLU	A	441	15.998	25.285	-1.375	1.00	65.36
ATOM	3010	CB	GLU	A	441	16.229	25.847	-4.815	1.00	67.99
ATOM	3011	CG	GLU	A	441	16.500	24.745	-5.822	1.00	70.98
ATOM	3012	CD	GLU	A	441	17.353	25.228	-6.981	1.00	72.23
ATOM	3013	OE1	GLU	A	441	18.507	25.646	-6.742	1.00	73.24
ATOM	3014	OE2	GLU	A	441	16.867	25.194	-8.132	1.00	73.30
ATOM	3015	N	ASP	A	442	16.170	23.585	-2.896	1.00	61.29
ATOM	3016	CA	ASP	A	442	15.519	22.616	-1.986	1.00	58.37
ATOM	3017	C	ASP	A	442	16.504	21.966	-1.018	1.00	55.47
ATOM	3018	O	ASP	A	442	16.615	20.704	-0.950	1.00	54.59
ATOM	3019	CB	ASP	A	442	14.800	21.530	-2.785	1.00	59.93
ATOM	3020	CG	ASP	A	442	13.298	21.616	-2.646	1.00	60.90
ATOM	3021	OD1	ASP	A	442	12.689	22.478	-3.312	1.00	61.34
ATOM	3022	OD2	ASP	A	442	12.729	20.832	-1.854	1.00	61.81
ATOM	3023	N	CYS	A	443	17.207	22.790	-0.252	1.00	51.31
ATOM	3024	CA	CYS	A	443	18.200	22.281	0.713	1.00	47.79
ATOM	3025	C	CYS	A	443	17.635	22.156	2.121	1.00	46.40
ATOM	3026	O	CYS	A	443	18.168	21.373	2.965	1.00	44.04
ATOM	3027	CB	CYS	A	443	19.421	23.198	0.713	1.00	48.61
ATOM	3028	SG	CYS	A	443	20.176	23.339	-0.939	1.00	46.95
ATOM	3029	N	GLY	A	444	16.566	22.895	2.395	1.00	45.40
ATOM	3030	CA	GLY	A	444	15.953	22.846	3.709	1.00	45.06
ATOM	3031	C	GLY	A	444	15.011	21.673	3.899	1.00	45.25
ATOM	3032	O	GLY	A	444	14.271	21.264	2.952	1.00	44.97
ATOM	3033	N	TYR	A	445	15.018	21.109	5.101	1.00	44.97
ATOM	3034	CA	TYR	A	445	14.140	19.968	5.421	1.00	44.48

ATOM	3035	C	TYR	A	445	12.778	20.467	5.882	1.00	45.23
ATOM	3036	O	TYR	A	445	12.662	21.558	6.530	1.00	44.57
ATOM	3037	CB	TYR	A	445	14.801	19.172	6.531	1.00	43.11
ATOM	3038	CG	TYR	A	445	13.918	17.997	6.871	1.00	42.75
ATOM	3039	CD1	TYR	A	445	13.846	16.905	6.010	1.00	42.58
ATOM	3040	CD2	TYR	A	445	13.170	17.998	8.049	1.00	42.27
ATOM	3041	CE1	TYR	A	445	13.042	15.820	6.327	1.00	41.99
ATOM	3042	CE2	TYR	A	445	12.358	16.917	8.360	1.00	43.20
ATOM	3043	CZ	TYR	A	445	12.289	15.835	7.503	1.00	41.98
ATOM	3044	OH	TYR	A	445	11.490	14.751	7.810	1.00	20.00
ATOM	3045	N	ASN	A	446	11.746	19.699	5.550	1.00	45.69
ATOM	3046	CA	ASN	A	446	10.359	20.012	5.947	1.00	48.64
ATOM	3047	C	ASN	A	446	9.776	18.726	6.524	1.00	50.90
ATOM	3048	O	ASN	A	446	9.894	17.625	5.896	1.00	51.59
ATOM	3049	CB	ASN	A	446	9.537	20.470	4.738	1.00	48.19
ATOM	3050	CG	ASN	A	446	9.975	21.827	4.213	1.00	48.18
ATOM	3051	OD1	ASN	A	446	9.926	22.858	4.950	1.00	48.63
ATOM	3052	ND2	ASN	A	446	10.403	21.867	2.957	1.00	48.04
ATOM	3053	N	ILE	A	447	9.165	18.826	7.700	1.00	53.94
ATOM	3054	CA	ILE	A	447	8.569	17.650	8.388	1.00	55.99
ATOM	3055	C	ILE	A	447	7.720	16.772	7.463	1.00	57.01
ATOM	3056	O	ILE	A	447	7.449	17.195	6.318	1.00	58.11
ATOM	3057	CB	ILE	A	447	7.699	18.105	9.577	1.00	55.86
ATOM	3058	CG1	ILE	A	447	8.488	19.086	10.450	1.00	56.28
ATOM	3059	CG2	ILE	A	447	7.267	16.900	10.406	1.00	56.92
ATOM	3060	CD1	ILE	A	447	9.759	18.505	11.037	1.00	55.79
ATOM	3061	OXT	ILE	A	447	7.328	15.666	7.895	1.00	57.55
ATOM	3062	N	SER	P	1	35.528	15.672	28.238	1.00	37.61
ATOM	3063	CA	SER	P	1	34.172	16.082	28.590	1.00	36.72
ATOM	3064	C	SER	P	1	33.508	16.863	27.450	1.00	34.75
ATOM	3065	O	SER	P	1	34.132	17.643	26.742	1.00	36.46
ATOM	3066	CB	SER	P	1	34.248	16.949	29.848	1.00	37.77
ATOM	3067	OG	SER	P	1	33.152	17.865	29.853	1.00	40.82
ATOM	3068	N	GLU	P	2	32.203	16.601	27.257	1.00	32.86
ATOM	3069	CA	GLU	P	2	31.513	17.216	26.129	1.00	32.80
ATOM	3070	C	GLU	P	2	30.218	17.906	26.552	1.00	31.23
ATOM	3071	O	GLU	P	2	29.435	17.401	27.348	1.00	31.31
ATOM	3072	CB	GLU	P	2	31.275	16.167	25.027	1.00	33.64
ATOM	3073	CG	GLU	P	2	31.096	17.096	23.826	1.00	37.41
ATOM	3074	CD	GLU	P	2	31.076	15.940	22.852	1.00	38.37
ATOM	3075	OE1	GLU	P	2	31.996	15.134	22.983	1.00	39.04
ATOM	3076	OE2	GLU	P	2	30.175	15.798	22.037	1.00	39.43
ATOM	3077	N	VAL	P	3	29.742	19.344	26.106	1.00	27.98
ATOM	3078	CA	VAL	P	3	28.367	19.820	26.101	1.00	26.44
ATOM	3079	C	VAL	P	3	27.717	19.598	24.735	1.00	26.26
ATOM	3080	O	VAL	P	3	28.371	19.580	23.701	1.00	25.48
ATOM	3081	CB	VAL	P	3	28.377	21.311	26.429	1.00	25.89
ATOM	3082	CG1	VAL	P	3	28.684	21.516	27.911	1.00	27.07
ATOM	3083	CG2	VAL	P	3	29.431	22.012	25.594	1.00	23.97
ATOM	3084	N	ASN	P	4	26.361	19.591	25.174	1.00	25.89
ATOM	3085	CA	ASN	P	4	25.421	19.254	24.075	1.00	26.64
ATOM	3086	C	ASN	P	4	24.027	19.825	24.452	1.00	26.87
ATOM	3087	O	ASN	P	4	23.116	19.163	25.077	1.00	27.10
ATOM	3088	CB	ASN	P	4	25.349	17.766	23.876	1.00	27.95
ATOM	3089	CG	ASN	P	4	26.498	17.245	22.971	1.00	29.39
ATOM	3090	OD1	ASN	P	4	26.499	17.409	21.723	1.00	31.90
ATOM	3091	ND2	ASN	P	4	27.489	16.617	23.603	1.00	31.97
ATOM	3092	N	STA	P	5	24.115	21.101	24.323	1.00	25.26
ATOM	3093	CA	STA	P	5	22.965	21.865	24.929	1.00	25.83
ATOM	3094	CB	STA	P	5	23.683	22.681	26.021	1.00	27.28
ATOM	3095	CG	STA	P	5	24.378	22.057	27.197	1.00	28.07
ATOM	3096	CD1	STA	P	5	25.002	23.077	28.182	1.00	27.46

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ATOM   3097  CD2 STA P   5      23.280  21.130  27.828  1.00 25.47
ATOM   3098  CH  STA P   5      22.223  22.851  23.940  1.00 25.86
ATOM   3099  OH  STA P   5      23.028  23.679  23.298  1.00 25.23
ATOM   3100  CM  STA P   5      21.372  21.980  23.048  1.00 27.11
ATOM   3101  C   STA P   5      20.420  21.340  24.125  1.00 27.81
ATOM   3102  O   STA P   5      20.241  20.065  24.095  1.00 25.70
ATOM   3103  N   VAL P   6      19.339  22.479  23.764  1.00 26.04
ATOM   3104  CA  VAL P   6      18.037  21.953  24.156  1.00 27.12
ATOM   3105  C   VAL P   6      17.496  20.965  23.121  1.00 27.36
ATOM   3106  O   VAL P   6      17.795  21.029  21.936  1.00 26.97
ATOM   3107  CB  VAL P   6      17.073  23.130  24.312  1.00 27.18
ATOM   3108  CG1 VAL P   6      16.433  23.463  22.965  1.00 26.70
ATOM   3109  CG2 VAL P   6      15.985  22.781  25.311  1.00 28.74
ATOM   3110  N   ALA P   7      16.702  19.998  23.617  1.00 28.68
ATOM   3111  CA  ALA P   7      16.158  18.986  22.720  1.00 32.14
ATOM   3112  C   ALA P   7      14.774  19.377  22.197  1.00 32.99
ATOM   3113  O   ALA P   7      14.040  20.149  22.801  1.00 32.08
ATOM   3114  CB  ALA P   7      16.072  17.666  23.489  1.00 31.38
ATOM   3115  N   GLU P   8      14.443  18.843  21.007  1.00 36.10
ATOM   3116  CA  GLU P   8      13.144  19.143  20.418  1.00 39.90
ATOM   3117  C   GLU P   8      12.012  18.425  21.158  1.00 41.72
ATOM   3118  O   GLU P   8      12.189  17.359  21.733  1.00 41.52
ATOM   3119  CB  GLU P   8      13.172  18.705  18.952  1.00 39.88
ATOM   3120  CG  GLU P   8      14.037  19.626  18.090  1.00 41.02
ATOM   3121  CD  GLU P   8      13.896  19.235  16.637  1.00 41.83
ATOM   3122  OE1 GLU P   8      14.911  19.052  15.979  1.00 41.60
ATOM   3123  OE2 GLU P   8      12.765  19.124  16.169  1.00 41.88
ATOM   3124  N   PHE P   9      10.811  18.986  21.162  1.00 45.62
ATOM   3125  CA  PHE P   9       9.677  18.356  21.865  1.00 49.63
ATOM   3126  C   PHE P   9       9.382  16.960  21.337  1.00 50.61
ATOM   3127  O   PHE P   9       9.156  16.839  20.116  1.00 51.38
ATOM   3128  CB  PHE P   9       8.451  19.245  21.670  1.00 50.65
ATOM   3129  CG  PHE P   9       8.607  20.501  22.499  1.00 52.48
ATOM   3130  CD1 PHE P   9       8.278  20.493  23.849  1.00 52.80
ATOM   3131  CD2 PHE P   9       9.073  21.659  21.899  1.00 53.12
ATOM   3132  CE1 PHE P   9       8.420  21.651  24.600  1.00 53.74
ATOM   3133  CE2 PHE P   9       9.215  22.817  22.659  1.00 53.61
ATOM   3134  CZ  PHE P   9       8.890  22.817  24.010  1.00 54.24
ATOM   3135  OXT PHE P   9       9.383  16.011  22.152  1.00 51.56
ATOM   3136  OH2 TIP C   2      37.673   4.149  14.933  1.00 18.73
ATOM   3137  OH2 TIP C   3      37.999  19.019  28.545  1.00 20.36
ATOM   3138  OH2 TIP C  12      46.550  23.555   9.446  1.00 16.05
ATOM   3139  OH2 TIP C  14      18.354  26.505  28.719  1.00 14.14
ATOM   3140  OH2 TIP C  15      33.073  10.884  15.835  1.00 14.30
ATOM   3141  OH2 TIP C  16      15.032  34.698  31.070  1.00 11.96
ATOM   3142  OH2 TIP C  17       7.170  35.908  33.277  1.00 16.70
ATOM   3143  OH2 TIP C  19      16.624  32.704  28.166  1.00 15.10
ATOM   3144  OH2 TIP C  20      35.078  42.552  29.609  1.00 19.72
ATOM   3145  OH2 TIP C  21      40.457  30.360  27.755  1.00 16.31
ATOM   3146  OH2 TIP C  22      52.263  20.430   9.725  1.00 20.11
ATOM   3147  OH2 TIP C  23      20.720  20.412  14.822  1.00 12.68
ATOM   3148  OH2 TIP C  24      33.413  15.317  -5.393  1.00 15.90
ATOM   3149  OH2 TIP C  25      38.275  25.072  23.469  1.00 13.40
ATOM   3150  OH2 TIP C  27      16.591  21.729   7.186  1.00 19.86
ATOM   3151  OH2 TIP C  28      21.798  19.346  19.780  1.00 14.31
ATOM   3152  OH2 TIP C  29      17.533  34.724  25.177  1.00 16.69
ATOM   3153  OH2 TIP C  30      29.162  27.768  25.821  1.00 19.19
ATOM   3154  OH2 TIP C  31      40.631  28.021  16.946  1.00 14.53
ATOM   3155  OH2 TIP C  32      32.428  32.415  17.998  1.00 10.42
ATOM   3156  OH2 TIP C  33      11.884  34.798  21.161  1.00 23.00
ATOM   3157  OH2 TIP C  34      27.837  25.769  -5.173  1.00 33.18
ATOM   3158  OH2 TIP C  35      12.372  31.279  28.339  1.00 16.96
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ATOM	3159	OH2	TIP	C	36	39.263	28.648	25.755	1.00 9.84
ATOM	3160	OH2	TIP	C	40	38.924	30.840	30.171	1.00 13.35
ATOM	3161	OH2	TIP	C	41	18.085	18.989	18.858	1.00 16.60
ATOM	3162	OH2	TIP	C	42	7.300	35.692	30.168	1.00 19.22
ATOM	3163	OH2	TIP	C	43	14.250	32.017	30.405	1.00 18.32
ATOM	3164	OH2	TIP	C	44	37.440	22.761	1.333	1.00 23.96
ATOM	3165	OH2	TIP	C	45	29.932	39.949	32.969	1.00 22.64
ATOM	3166	OH2	TIP	C	46	29.433	17.902	20.935	1.00 16.15
ATOM	3167	OH2	TIP	C	47	53.536	22.468	21.774	1.00 21.62
ATOM	3168	OH2	TIP	C	48	40.180	15.699	-0.272	1.00 12.15
ATOM	3169	OH2	TIP	C	49	14.955	25.973	25.745	1.00 11.98
ATOM	3170	OH2	TIP	C	50	38.595	6.527	3.885	1.00 23.66
ATOM	3171	OH2	TIP	C	51	48.551	24.793	17.574	1.00 18.30
ATOM	3172	OH2	TIP	C	52	20.747	27.407	17.869	1.00 8.25
ATOM	3173	OH2	TIP	C	53	26.489	18.730	30.746	1.00 26.59
ATOM	3174	OH2	TIP	C	54	38.723	11.162	19.249	1.00 11.49
ATOM	3175	OH2	TIP	C	55	33.881	26.191	31.382	1.00 19.21
ATOM	3176	OH2	TIP	C	56	13.322	31.213	40.027	1.00 15.61
ATOM	3177	OH2	TIP	C	57	19.497	16.134	41.439	1.00 26.82
ATOM	3178	OH2	TIP	C	58	38.469	37.062	5.695	1.00 23.10
ATOM	3179	OH2	TIP	C	59	45.575	15.894	3.122	1.00 18.45
ATOM	3180	OH2	TIP	C	60	39.615	25.333	-1.743	1.00 20.09
ATOM	3181	OH2	TIP	C	61	32.158	37.928	32.431	1.00 12.17
ATOM	3182	OH2	TIP	C	62	46.793	19.609	22.823	1.00 19.81
ATOM	3183	OH2	TIP	C	63	24.847	37.031	-0.659	1.00 29.98
ATOM	3184	OH2	TIP	C	64	45.957	18.715	3.836	1.00 18.88
ATOM	3185	OH2	TIP	C	65	36.189	33.100	17.653	1.00 10.63
ATOM	3186	OH2	TIP	C	66	31.177	25.020	24.150	1.00 28.40
ATOM	3187	OH2	TIP	C	67	46.181	23.210	18.466	1.00 20.41
ATOM	3188	OH2	TIP	C	68	21.756	10.923	7.943	1.00 22.80
ATOM	3189	OH2	TIP	C	69	12.936	36.695	30.481	1.00 17.63
ATOM	3190	OH2	TIP	C	70	33.713	44.843	8.382	1.00 30.49
ATOM	3191	OH2	TIP	C	71	21.051	41.550	39.982	1.00 31.15
ATOM	3192	OH2	TIP	C	72	26.815	38.732	3.198	1.00 22.61
ATOM	3193	OH2	TIP	C	73	41.656	24.820	21.177	1.00 19.69
ATOM	3194	OH2	TIP	C	74	25.521	30.139	47.617	1.00 31.08
ATOM	3195	OH2	TIP	C	75	20.497	46.537	15.336	1.00 29.67
ATOM	3196	OH2	TIP	C	76	7.708	28.422	41.027	1.00 26.00
ATOM	3197	OH2	TIP	C	77	25.650	18.585	27.821	1.00 17.30
ATOM	3198	OH2	TIP	C	78	35.124	16.582	21.374	1.00 15.44
ATOM	3199	OH2	TIP	C	79	16.806	29.258	45.952	1.00 22.64
ATOM	3200	OH2	TIP	C	80	29.365	7.305	14.767	1.00 28.00
ATOM	3201	OH2	TIP	C	81	36.259	9.577	-0.018	1.00 36.72
ATOM	3202	OH2	TIP	C	82	5.598	37.375	35.367	1.00 29.64
ATOM	3203	OH2	TIP	C	83	14.256	22.267	9.863	1.00 20.30
ATOM	3204	OH2	TIP	C	84	34.533	14.826	41.318	1.00 35.70
ATOM	3205	OH2	TIP	C	85	14.253	38.931	17.469	1.00 22.15
ATOM	3206	OH2	TIP	C	86	40.762	43.633	8.075	1.00 32.27
ATOM	3207	OH2	TIP	C	87	20.139	38.471	47.202	1.00 19.79
ATOM	3208	OH2	TIP	C	88	49.003	25.388	14.809	1.00 16.95
ATOM	3209	OH2	TIP	C	89	48.376	21.580	21.346	1.00 26.51
ATOM	3210	OH2	TIP	C	90	38.281	15.314	27.561	1.00 34.16
ATOM	3211	OH2	TIP	C	91	8.631	39.984	34.095	1.00 41.37
ATOM	3212	OH2	TIP	C	92	50.906	23.612	20.744	1.00 52.18
ATOM	3213	OH2	TIP	C	93	53.785	20.060	24.538	1.00 24.16
ATOM	3214	OH2	TIP	C	94	24.823	42.619	11.579	1.00 21.18
ATOM	3215	OH2	TIP	C	95	25.075	45.083	6.146	1.00 38.65
ATOM	3216	OH2	TIP	C	96	40.830	25.584	18.443	1.00 18.31
ATOM	3217	OH2	TIP	C	97	43.416	22.239	18.182	1.00 19.16
ATOM	3218	OH2	TIP	C	98	13.417	34.174	40.223	1.00 31.15
ATOM	3219	OH2	TIP	C	99	33.278	34.940	35.258	1.00 19.39
ATOM	3220	OH2	TIP	C	100	16.214	11.125	16.638	1.00 44.74

ATOM	3221	OH2	TIP	C	101	53.364	20.723	14.579	1.00 34.15
ATOM	3222	OH2	TIP	C	102	49.883	22.898	7.975	1.00 17.76
ATOM	3223	OH2	TIP	C	103	23.025	15.361	39.364	1.00 32.71
ATOM	3224	OH2	TIP	C	104	9.989	41.920	29.368	1.00 18.54
ATOM	3225	OH2	TIP	C	105	40.434	26.276	24.857	1.00 17.36
ATOM	3226	OH2	TIP	C	106	20.997	29.964	6.095	1.00 20.90
ATOM	3227	OH2	TIP	C	107	27.762	47.336	16.035	1.00 24.48
ATOM	3228	OH2	TIP	C	108	49.284	22.771	5.126	1.00 18.73
ATOM	3229	OH2	TIP	C	109	48.838	23.239	29.592	1.00 33.97
ATOM	3230	OH2	TIP	C	110	28.582	23.099	35.349	1.00 20.25
ATOM	3231	OH2	TIP	C	111	32.528	35.162	39.110	1.00 29.39
ATOM	3232	OH2	TIP	C	112	41.404	21.066	27.696	1.00 29.24
ATOM	3233	OH2	TIP	C	113	41.566	30.795	24.916	1.00 29.04
ATOM	3234	OH2	TIP	C	114	38.888	34.349	4.634	1.00 19.24
ATOM	3235	OH2	TIP	C	115	21.524	13.318	6.181	1.00 21.83
ATOM	3236	OH2	TIP	C	116	20.262	44.365	41.166	1.00 51.68
ATOM	3237	OH2	TIP	C	117	40.866	37.586	7.262	1.00 26.48
ATOM	3238	OH2	TIP	C	118	24.269	19.013	20.381	1.00 20.56
ATOM	3239	OH2	TIP	C	119	14.796	40.366	21.026	1.00 26.21
ATOM	3240	OH2	TIP	C	120	40.271	21.968	24.452	1.00 22.99
ATOM	3241	OH2	TIP	C	121	27.256	8.206	3.568	1.00 32.16
ATOM	3242	OH2	TIP	C	122	38.453	23.426	21.155	1.00 20.65
ATOM	3243	OH2	TIP	C	123	39.489	30.192	18.787	1.00 19.64
ATOM	3244	OH2	TIP	C	124	49.479	24.877	3.120	1.00 15.38
ATOM	3245	OH2	TIP	C	125	23.534	17.922	36.838	1.00 21.55
ATOM	3246	OH2	TIP	C	126	24.481	13.568	37.531	1.00 33.00
ATOM	3247	OH2	TIP	C	127	27.515	37.075	45.132	1.00 32.65
ATOM	3248	OH2	TIP	C	128	20.903	11.530	10.774	1.00 25.13
ATOM	3249	OH2	TIP	C	129	16.996	37.117	6.834	1.00 26.72
ATOM	3250	OH2	TIP	C	130	42.280	39.848	5.806	1.00 39.08
ATOM	3251	OH2	TIP	C	131	15.426	37.238	14.643	1.00 27.36
ATOM	3252	OH2	TIP	C	132	47.740	29.973	16.321	1.00 27.58
ATOM	3253	OH2	TIP	C	133	52.162	19.864	18.278	1.00 19.10
ATOM	3254	OH2	TIP	C	134	47.805	11.416	4.529	1.00 30.40
ATOM	3255	OH2	TIP	C	135	20.920	22.905	41.964	1.00 23.80
ATOM	3256	OH2	TIP	C	136	27.784	19.013	-1.506	1.00 28.71
ATOM	3257	OH2	TIP	C	137	25.506	36.437	2.115	1.00 19.53
ATOM	3258	OH2	TIP	C	138	6.347	36.058	44.801	1.00 30.54
ATOM	3259	OH2	TIP	C	139	18.428	23.862	8.397	1.00 19.65
ATOM	3260	OH2	TIP	C	140	56.631	14.945	24.048	1.00 29.26
ATOM	3261	OH2	TIP	C	141	36.045	33.381	-3.424	1.00 39.63
ATOM	3262	OH2	TIP	C	142	20.242	14.180	11.802	1.00 31.49
ATOM	3263	OH2	TIP	C	143	8.614	22.301	31.526	1.00 30.94
ATOM	3264	OH2	TIP	C	144	8.697	38.736	31.440	1.00 44.64
ATOM	3265	OH2	TIP	C	145	21.002	20.115	40.621	1.00 23.34
ATOM	3266	OH2	TIP	C	146	36.343	37.533	7.628	1.00 25.43
ATOM	3267	OH2	TIP	C	147	13.944	44.970	51.125	1.00 40.01
ATOM	3268	OH2	TIP	C	148	12.509	22.964	23.735	1.00 33.44
ATOM	3269	OH2	TIP	C	149	32.555	6.398	6.686	1.00 30.50
ATOM	3270	OH2	TIP	C	150	11.123	30.018	41.695	1.00 29.12
ATOM	3271	OH2	TIP	C	151	20.406	19.454	17.419	1.00 26.72
ATOM	3272	OH2	TIP	C	152	37.729	21.375	25.750	1.00 27.16
ATOM	3273	OH2	TIP	C	153	36.922	28.170	33.507	1.00 42.28
ATOM	3274	OH2	TIP	C	154	13.904	29.766	32.277	1.00 19.72
ATOM	3275	OH2	TIP	C	155	54.556	19.732	11.775	1.00 37.67
ATOM	3276	OH2	TIP	C	156	14.999	28.327	48.310	1.00 40.64
ATOM	3277	OH2	TIP	C	157	19.001	46.759	12.106	1.00 40.48
ATOM	3278	OH2	TIP	C	158	22.361	9.339	13.691	1.00 44.57
ATOM	3279	OH2	TIP	C	159	26.097	16.601	36.996	1.00 27.61
ATOM	3280	OH2	TIP	C	160	51.862	24.669	14.501	1.00 39.22
ATOM	3281	OH2	TIP	C	161	42.713	33.316	38.299	1.00 37.21
ATOM	3282	OH2	TIP	C	162	32.074	43.316	6.583	1.00 32.14

ATOM	3283	OH2	TIP	C	163	44.434	22.056	2.693	1.00	44.76
ATOM	3284	OH2	TIP	C	164	24.074	33.090	45.770	1.00	26.95
ATOM	3285	OH2	TIP	C	165	12.289	35.656	48.500	1.00	33.30
ATOM	3286	OH2	TIP	C	166	19.499	27.253	51.538	1.00	48.93
ATOM	3287	OH2	TIP	C	167	28.896	14.390	20.410	1.00	32.12
ATOM	3288	OH2	TIP	C	168	7.799	34.543	25.107	1.00	34.11
ATOM	3289	OH2	TIP	C	169	41.359	33.697	5.939	1.00	29.72
ATOM	3290	OH2	TIP	C	170	26.378	23.008	46.449	1.00	37.54
ATOM	3291	OH2	TIP	C	171	10.530	41.770	49.010	1.00	34.66
ATOM	3292	OH2	TIP	C	172	41.154	5.586	4.533	1.00	25.18
ATOM	3293	OH2	TIP	C	173	17.462	11.487	4.521	1.00	46.32
ATOM	3294	OH2	TIP	C	174	7.600	39.527	37.113	1.00	36.37
ATOM	3295	OH2	TIP	C	175	3.552	23.235	37.583	1.00	39.37
ATOM	3296	OH2	TIP	C	176	32.818	21.891	40.191	1.00	36.81
ATOM	3297	OH2	TIP	C	177	30.404	26.159	40.588	1.00	38.22
ATOM	3298	OH2	TIP	C	178	16.691	29.183	54.400	1.00	39.76
ATOM	3299	OH2	TIP	C	179	16.247	47.986	22.417	1.00	32.19
ATOM	3300	OH2	TIP	C	180	37.394	44.558	11.594	1.00	39.03
ATOM	3301	OH2	TIP	C	181	53.552	27.209	11.822	1.00	47.97
ATOM	3302	OH2	TIP	C	182	10.503	32.709	12.025	1.00	38.41
ATOM	3303	OH2	TIP	C	183	17.985	14.916	28.259	1.00	36.86
ATOM	3304	OH2	TIP	C	184	25.047	45.446	12.174	1.00	49.92
ATOM	3305	OH2	TIP	C	185	16.402	15.741	36.532	1.00	40.29
ATOM	3306	OH2	TIP	C	186	51.364	22.471	17.335	1.00	28.11
ATOM	3307	OH2	TIP	C	187	25.633	28.369	50.282	1.00	42.57
ATOM	3308	OH2	TIP	C	188	35.183	14.816	0.037	1.00	36.60
ATOM	3309	OH2	TIP	C	189	8.318	26.536	23.386	1.00	44.75
ATOM	3310	OH2	TIP	C	190	47.893	17.794	24.745	1.00	42.51
ATOM	3311	OH2	TIP	C	191	2.728	32.293	36.650	1.00	38.36
ATOM	3312	OH2	TIP	C	192	30.315	9.929	15.860	1.00	39.58
ATOM	3313	OH2	TIP	C	193	29.613	40.378	2.225	1.00	41.26
ATOM	3314	OH2	TIP	C	194	14.241	43.934	16.316	1.00	43.60
ATOM	3315	OH2	TIP	C	195	48.673	31.215	7.801	1.00	32.67
ATOM	3316	OH2	TIP	C	196	10.948	21.963	18.969	1.00	41.87
ATOM	3317	OH2	TIP	C	197	37.378	39.077	3.714	1.00	35.77
ATOM	3318	OH2	TIP	C	198	24.488	11.993	21.654	1.00	38.05
ATOM	3319	OH2	TIP	C	199	47.986	31.378	4.946	1.00	48.02
ATOM	3320	OH2	TIP	C	200	15.373	46.520	15.659	1.00	45.30
ATOM	3321	OH2	TIP	C	201	29.464	40.417	40.154	1.00	40.62
ATOM	3322	OH2	TIP	C	202	56.018	18.652	7.189	1.00	43.28
ATOM	3323	OH2	TIP	C	203	36.508	17.526	41.765	1.00	61.21
ATOM	3324	OH2	TIP	C	204	36.132	36.523	-0.637	1.00	43.56
ATOM	3325	OH2	TIP	C	205	9.832	29.974	46.230	1.00	47.33
ATOM	3326	OH2	TIP	C	206	12.086	37.731	18.949	1.00	44.12
ATOM	3327	OH2	TIP	C	207	4.729	26.744	22.711	1.00	40.03
ATOM	3328	OH2	TIP	C	208	9.555	36.540	23.357	1.00	46.94
ATOM	3329	OH2	TIP	C	209	23.046	47.732	4.343	1.00	48.13
ATOM	3330	OH2	TIP	C	210	39.932	44.592	5.460	1.00	64.51
ATOM	3331	OH2	TIP	C	211	17.996	41.071	6.267	1.00	48.35
ATOM	3332	OH2	TIP	C	212	17.866	46.493	17.139	1.00	39.09
ATOM	3333	OH2	TIP	C	213	55.520	11.908	17.658	1.00	43.06
ATOM	3334	OH2	TIP	C	214	3.059	35.093	42.826	1.00	38.97
ATOM	3335	OH2	TIP	C	215	31.593	14.910	43.677	1.00	44.01
ATOM	3336	OH2	TIP	C	216	33.045	23.673	44.607	1.00	45.50
ATOM	3337	OH2	TIP	C	217	42.870	35.555	7.510	1.00	29.79
ATOM	3338	OH2	TIP	C	218	4.112	25.648	42.564	1.00	56.65
ATOM	3339	OH2	TIP	C	219	48.260	8.547	20.446	1.00	47.85
ATOM	3340	OH2	TIP	C	220	-0.925	31.171	41.173	1.00	36.99
ATOM	3341	OH2	TIP	C	221	41.791	22.878	0.132	1.00	56.14
ATOM	3342	OH2	TIP	C	222	7.088	25.685	41.540	1.00	47.43
ATOM	3343	OH2	TIP	C	223	24.815	4.785	13.582	1.00	47.96
ATOM	3344	OH2	TIP	C	224	40.690	4.520	15.174	1.00	48.76

ATOM	3345	OH2	TIP	C	225	10.029	32.425	18.562	1.00	36.30
ATOM	3346	OH2	TIP	C	226	22.346	37.737	48.941	1.00	34.15
ATOM	3347	OH2	TIP	C	227	16.274	17.012	19.693	1.00	27.63
ATOM	3348	OH2	TIP	C	228	35.332	13.692	20.375	1.00	37.59
ATOM	3349	OH2	TIP	C	229	41.228	36.673	22.908	1.00	51.58
ATOM	3350	OH2	TIP	C	230	17.416	42.030	50.226	1.00	47.63
ATOM	3351	OH2	TIP	C	231	18.428	39.213	52.835	1.00	40.43
ATOM	3352	OH2	TIP	C	232	42.243	43.386	25.548	1.00	48.60
ATOM	3353	OH2	TIP	C	233	14.081	18.701	0.364	1.00	32.87
ATOM	3354	OH2	TIP	C	234	41.421	41.332	28.531	1.00	54.67
ATOM	3355	OH2	TIP	C	235	42.772	36.396	11.892	1.00	41.24
ATOM	3356	OH2	TIP	C	236	13.068	13.733	28.653	1.00	42.66
ATOM	3357	OH2	TIP	C	237	10.850	26.738	7.811	1.00	40.46
ATOM	3358	OH2	TIP	C	238	16.253	20.926	45.776	1.00	44.60
ATOM	3359	OH2	TIP	C	239	32.681	31.139	43.220	1.00	42.20
ATOM	3360	OH2	TIP	C	240	56.267	22.254	9.280	1.00	52.44
ATOM	3361	OH2	TIP	C	241	12.553	25.304	9.942	1.00	38.77
ATOM	3362	OH2	TIP	C	242	50.727	9.516	16.775	1.00	33.38
ATOM	3363	OH2	TIP	C	243	31.871	41.347	0.512	1.00	47.78
ATOM	3364	OH2	TIP	C	244	10.008	45.092	37.807	1.00	39.52
ATOM	3365	OH2	TIP	C	245	14.551	39.030	6.708	1.00	44.26
ATOM	3366	OH2	TIP	C	246	26.955	18.903	-5.135	1.00	42.54
ATOM	3367	OH2	TIP	C	247	39.916	22.478	18.854	1.00	33.22
ATOM	3368	OH2	TIP	C	248	40.431	40.824	22.426	1.00	35.58
ATOM	3369	OH2	TIP	C	249	52.081	23.408	10.759	1.00	42.53
ATOM	3370	OH2	TIP	C	250	12.078	16.710	24.149	1.00	32.37
ATOM	3371	OH2	TIP	C	251	54.111	15.908	8.256	1.00	44.58
ATOM	3372	OH2	TIP	C	252	33.950	12.827	-1.753	1.00	27.02
ATOM	3373	OH2	TIP	C	253	-0.775	26.703	40.353	1.00	43.64
ATOM	3374	OH2	TIP	C	254	1.937	33.711	40.561	1.00	42.67
ATOM	3375	OH2	TIP	C	255	8.008	24.066	18.824	1.00	51.45
ATOM	3376	OH2	TIP	C	256	11.765	27.465	3.635	1.00	47.34
ATOM	3377	OH2	TIP	C	257	27.863	43.878	9.233	1.00	32.44
ATOM	3378	OH2	TIP	C	258	18.655	30.114	4.303	1.00	33.13
ATOM	3379	OH2	TIP	C	259	21.592	19.085	-3.960	1.00	39.86
ATOM	3380	OH2	TIP	C	260	41.876	24.067	25.906	1.00	26.34
ATOM	3381	OH2	TIP	C	261	46.651	10.240	2.171	1.00	44.38
ATOM	3382	OH2	TIP	C	262	32.536	15.827	32.477	1.00	43.28
ATOM	3383	OH2	TIP	C	263	12.479	39.205	50.359	1.00	47.33
ATOM	3384	OH2	TIP	C	264	0.850	27.980	38.316	1.00	43.45
ATOM	3385	OH2	TIP	C	265	49.605	7.356	18.061	1.00	66.01
ATOM	3386	OH2	TIP	C	266	30.177	40.365	-3.235	1.00	44.45
ATOM	3387	OH2	TIP	C	267	39.818	12.364	0.512	1.00	48.84
ATOM	3388	OH2	TIP	C	268	38.149	44.716	27.884	1.00	51.18
ATOM	3389	OH2	TIP	C	269	37.156	37.062	30.528	1.00	35.17
ATOM	3390	OH2	TIP	C	270	51.808	7.097	12.435	1.00	51.69
ATOM	3391	OH2	TIP	C	271	54.351	12.626	12.471	1.00	47.45
ATOM	3392	OH2	TIP	C	272	50.835	31.155	13.092	1.00	55.05
ATOM	3393	OH2	TIP	C	273	12.159	35.313	52.133	1.00	52.38
ATOM	3394	OH2	TIP	C	274	21.002	44.489	13.037	1.00	39.70
ATOM	3395	OH2	TIP	C	275	37.936	23.627	34.221	1.00	48.56
ATOM	3396	OH2	TIP	C	276	45.844	30.935	31.365	1.00	43.24
ATOM	3397	OH2	TIP	C	277	38.831	48.015	15.554	1.00	49.83
ATOM	3398	OH2	TIP	C	278	5.630	28.150	44.576	1.00	48.10
ATOM	3399	OH2	TIP	C	279	8.600	24.000	45.727	1.00	49.27
ATOM	3400	OH2	TIP	C	280	54.276	20.854	7.807	1.00	36.02
ATOM	3401	OH2	TIP	C	281	3.544	34.696	46.365	1.00	43.63
ATOM	3402	OH2	TIP	C	282	24.214	46.264	46.163	1.00	48.04
ATOM	3403	OH2	TIP	C	283	7.099	32.072	19.549	1.00	54.97
ATOM	3404	OH2	TIP	C	284	36.469	22.374	41.355	1.00	52.17
ATOM	3405	OH2	TIP	C	285	34.660	13.757	23.756	1.00	45.46
ATOM	3406	OH2	TIP	C	286	28.516	42.981	5.402	1.00	53.58

ATOM	3407	OH2	TIP	C	287	35.579	4.929	12.012	1.00 52.07
ATOM	3408	OH2	TIP	C	288	22.974	49.682	24.299	1.00 53.67
ATOM	3409	OH2	TIP	C	289	3.725	31.464	46.354	1.00 46.43
ATOM	3410	OH2	TIP	C	290	27.340	39.594	-2.191	1.00 56.89
ATOM	3411	OH2	TIP	C	291	33.413	34.856	32.335	1.00 31.78
ATOM	3412	OH2	TIP	C	292	43.340	7.715	8.063	1.00 43.53
ATOM	3413	OH2	TIP	C	293	28.243	21.392	-4.937	1.00 38.33
ATOM	3414	OH2	TIP	C	294	49.389	26.590	35.796	1.00 45.66
ATOM	3415	OH2	TIP	C	295	28.948	15.824	33.796	1.00 52.48
ATOM	3416	OH2	TIP	C	296	27.347	13.383	37.207	1.00 48.27
ATOM	3417	OH2	TIP	C	297	38.485	26.090	36.901	1.00 48.92
ATOM	3418	OH2	TIP	C	298	12.120	20.265	11.506	1.00 50.10
ATOM	3419	OH2	TIP	C	299	36.480	36.306	38.613	1.00 50.38
ATOM	3420	OH2	TIP	C	300	31.471	16.463	35.507	1.00 38.37
ATOM	3421	OH2	TIP	C	301	42.889	5.274	2.358	1.00 33.49
ATOM	3422	OH2	TIP	C	302	23.548	44.173	32.246	1.00 39.09
ATOM	3423	OH2	TIP	C	303	13.465	43.978	13.054	1.00 52.67
ATOM	3424	OH2	TIP	C	304	25.133	43.053	4.111	1.00 52.03
ATOM	3425	OH2	TIP	C	305	33.587	24.652	39.392	1.00 49.48
ATOM	3426	OH2	TIP	C	306	39.063	28.353	1.979	1.00 47.89
ATOM	3427	OH2	TIP	C	307	49.357	35.834	12.150	1.00 49.22
ATOM	3428	OH2	TIP	C	308	27.159	46.386	33.347	1.00 49.50
ATOM	3429	OH2	TIP	C	309	9.510	21.769	39.704	1.00 47.95
ATOM	3430	OH2	TIP	C	310	34.885	32.959	39.205	1.00 51.26
ATOM	3431	OH2	TIP	C	311	30.980	6.002	9.747	1.00 56.02
ATOM	3432	OH2	TIP	C	312	43.802	34.511	14.853	1.00 41.89
ATOM	3433	OH2	TIP	C	313	36.834	4.382	5.254	1.00 39.04
ATOM	3434	OH2	TIP	C	314	12.453	30.429	47.461	1.00 47.60
ATOM	3435	OH2	TIP	C	315	39.685	40.144	30.944	1.00 54.68
ATOM	3436	OH2	TIP	C	316	45.982	20.840	31.078	1.00 47.99
ATOM	3437	OH2	TIP	C	317	32.815	36.023	42.050	1.00 45.07
ATOM	3438	OH2	TIP	C	318	17.877	37.802	-3.699	1.00 56.30
ATOM	3439	OH2	TIP	C	319	53.681	9.633	16.525	1.00 55.34
ATOM	3440	OH2	TIP	C	320	21.577	43.070	52.229	1.00 49.54
ATOM	3441	OH2	TIP	C	321	6.139	45.122	36.565	1.00 44.40
ATOM	3442	OH2	TIP	C	322	34.695	13.561	26.782	1.00 45.99
ATOM	3443	OH2	TIP	C	323	17.990	33.946	-9.976	1.00 56.88
ATOM	3444	OH2	TIP	C	324	25.587	50.416	28.268	1.00 52.75
ATOM	3445	OH2	TIP	C	325	27.744	42.608	42.266	1.00 44.66
ATOM	3446	OH2	TIP	C	326	48.357	32.815	33.851	1.00 57.98
ATOM	3447	OH2	TIP	C	327	61.047	18.004	17.692	1.00 51.30
ATOM	3448	OH2	TIP	C	328	17.327	11.069	11.972	1.00 48.28
ATOM	3449	OH2	TIP	C	329	59.624	17.562	20.598	1.00 44.37
ATOM	3450	OH2	TIP	C	330	40.644	39.227	19.932	1.00 37.57
ATOM	3451	OH2	TIP	C	331	12.920	31.214	52.942	1.00 51.07
ATOM	3452	OH2	TIP	C	332	37.639	0.847	19.561	1.00 49.44
ATOM	3453	OH2	TIP	C	333	34.243	38.790	-3.251	1.00 54.21
ATOM	3454	OH2	TIP	C	334	24.216	47.874	6.983	1.00 50.90
ATOM	3455	OH2	TIP	C	335	15.324	34.797	6.670	1.00 45.25
ATOM	3456	OH2	TIP	C	336	18.474	15.525	21.402	1.00 34.12
ATOM	3457	OH2	TIP	C	337	40.048	8.873	26.818	1.00 49.89
ATOM	3458	OH2	TIP	C	338	32.472	13.331	20.523	1.00 29.86
ATOM	3459	OH2	TIP	C	339	57.778	14.167	30.422	1.00 49.76
ATOM	3460	OH2	TIP	C	340	46.651	35.476	13.375	1.00 56.48
ATOM	3461	OH2	TIP	C	341	15.427	13.237	3.552	1.00 57.25
ATOM	3462	OH2	TIP	C	342	40.349	38.972	3.722	1.00 65.27
ATOM	3463	OH2	TIP	C	343	8.685	28.945	15.205	1.00 59.60
ATOM	3464	OH2	TIP	C	344	11.958	41.585	22.587	1.00 37.18
ATOM	3465	OH2	TIP	C	345	9.054	20.498	28.914	1.00 42.95
ATOM	3466	OH2	TIP	C	346	20.086	20.088	46.913	1.00 42.03
ATOM	3467	OH2	TIP	C	347	40.370	35.093	2.009	1.00 49.35
ATOM	3468	OH2	TIP	C	348	41.948	4.327	12.147	1.00 50.59

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ATOM   3469  OH2 TIP C 349      23.518  45.701  40.287  1.00 39.79
ATOM   3470  OH2 TIP C 350      19.169  37.474   4.786  1.00 44.67
ATOM   3471  OH2 TIP C 351      32.946  39.184  41.062  1.00 57.56
ATOM   3472  OH2 TIP C 352      37.578  47.817  18.421  1.00 51.80
ATOM   3473  OH2 TIP C 353      15.391  43.820   7.645  1.00 58.15
ATOM   3474  OH2 TIP C 354      38.205  17.257  33.401  1.00 55.84
ATOM   3475  OH2 TIP C 355      43.224   1.565  14.606  1.00 41.12
ATOM   3476  OH2 TIP C 356      18.704  51.623  28.487  1.00 61.11
ATOM   3477  OH2 TIP C 357      46.033   5.813   0.173  1.00 43.43
ATOM   3478  OH2 TIP C 358      51.950  27.722  14.408  1.00 45.00
ATOM   3479  OH2 TIP C 359      46.825   2.427  15.714  1.00 52.68
ATOM   3480  OH2 TIP C 360      17.624  50.111  20.315  1.00 39.65
ATOM   3481  O   HOH C 361      27.534  15.877  26.687  1.00 20.00
ATOM   3482  O   HOH C 362      28.946  16.344  30.514  1.00 20.00
END
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/29387

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : G01N 33/483
US CL : 702/19

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 702/17, 435, 424.

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	ROSSJOHN et al. Crystal structure of the N-terminal, growth factor-like domain of Alzheimer amyloid precursor protein. Nature Structural Biology. April 1999, Vol 6. No. 4, pages 327-331, see entire document and especially page 330 in Methods.	1-2
Y	ZHANG Z. et al. Sequence-specific recognition of the interanalization motif of the Alzheimer's amyloid precursor protein by the X11 PTB domain. The EMBO Journal. 1997, Vol 16. No. 20, pages 6141-6150, see entire document and especially page 6147.	1-2
Y,P	MARCINKEVICIENE J. at al. Mechanism of Inhibition of beta-Site Amyloid Precursor Protein-cleaving Enzyme (BACE) by a Statine-based Peptide. The Journal of Biological Chemistry. 29 June 2001, Vol 276, No. 26, pages 23790-23794, see entire document.	1
Y	HYNES et al. X-ray Crystal Structure of the Protease Inhibitor Domain of Alzheimer's Amyloid beta-Protein Precursor. Biochemistry.1990, Vol 29, pages 10018-10022, especially page 10019.	1-2

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search
18 December 2001 (18.12.2001)

Date of mailing of the international search report
13 FEB 2002

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/29387

C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	BAILEY et al. X-ray-crystallographic studies of complexes of pepstatin A and a statine-containing human renin inhibitor with endothiapepsin. Biochem. J.1993, Vol 289, pages 363-371, especialy pages 365-366.	1-2
Y	SCHEIDIG et al. Crystal structures of bovin chymotrypsin and trypsin complexed to the inhibitor domain of Alzheimer's amyloid beta-protein precursor (APPI) and basic pancreatic trypsin inhibitor (BPTI): Engineering of inhibitors wth altered specificities. The Protein Society. September 1997, Vol 6, pages 1806-1824, see entire document and especially page 1820.	1-2
A	KOHNO et al. Thre-Dimentional Structure of the Amyloid beta Peptide (25-35) in Membrane-Mimicking Environment. Biochemistry. 1996, Vol 35, pages 16094-16104, see entire document.	1-2
A	VASSAR et al. Beta-Secretase Cleavage of Azheimer's Amyloid Precursor Protein by the Transmembrane Aspartic Protease BACE. Science. 22 October 1999, Vol 286, pages 735-741, see entire document.	1-2
A	HONG, L. et al. Structure of the Protease Domain of Memapsin 2(beta-Secretase) Complexed with Inhibitor. Science. 24 May 2000, Vol 290, No. 5489, pages 150-159, see entire document	1-2
A	SAUDER, M. et al. Modeling of substrate specifity of the Alzheimer's desease amyloid precursor protein beta-secretase. J. Mol. Biol. 2000, Vol 300, No. 2, pages 241-248, see entire document.	1-2

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/29387

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: 1 and 2

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest
☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/29387

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

The inventions listed as Groups I-II do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The inventions listed as Groups I-II do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Invention I and II are directed to different chemical and physical types regarding the critical limitations therein. For Group I, the critical feature is a crystallization of complex whereas for Group II the critical feature is the obtaining or synthesizing the agent. This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional examination fees must be paid.

Group I, claims 1-2, drawn to crystallized complex.

Group II, claims 24 and 27 drawn to method further comprising one of the steps: obtaining and synthesizing the agen. Claims 3-23, 25,26,28-30 are directed solely to information and are therefore excluded from search.

The International Searching Authority considers that the international application does not comply with the requirements of unity of invention (Rules 13.1, 13.2 and 13.3) for reasons indicated below:

The inventions listed as Groups I-II do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The inventions listed as Groups I-II do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Invention I and II are directed to different chemical and physical types regarding the critical limitations therein. For Group I, the critical feature is a crystallization of complex whereas for Group II the critical feature is the obtaining or synthesizing the agent.

Continuation of B. FIELDS SEARCHED Item 3:

WEST, STN, Non-patent-literature covering search terms: Cleaving Enzyme(BACE), crystallization, beta-Amyloid Precursor protein, 3-d structure of APP, Statine-based peptides.